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OM protein - protein search, using sw model

Run on: April 12, 2003, 22:29:49 ; Search time 9.77318 Seconds  
 (without alignments)  
 138.463 Million cell updates/sec

Title: US-09-380-546A-4  
 Perfect score: 1114  
 Sequence: 1 MSAEVHQVEEALDTDEKEM.....RMITPYAHCPDYLKILGNCSM 221

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*

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3: /cgns2_6_ptodata//2/pubpaa/US06_NEW_PUB.pep:*
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5: /cgns2_6_ptodata//2/pubpaa/US07_NEW_PUB.pep:*
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7: /cgns2_6_ptodata//2/pubpaa/PCT05_PUBCOMB.pep:*
8: /cgns2_6_ptodata//2/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1114	100.0	221	10 US-09-410-194-15	Sequence 15, Appl
2	1114	100.0	221	10 US-09-410-194-22	Sequence 22, Appl
3	1007	90.4	480	10 US-09-861-270-2	Sequence 2, Appl
4	1007	90.4	480	10 US-09-410-194-11	Sequence 11, Appl
5	1007	90.4	480	10 US-09-410-194-17	Sequence 17, Appl
6	713	64.0	481	10 US-09-194-12	Sequence 12, Appl
7	713	64.0	481	10 US-09-410-194-19	Sequence 19, Appl
8	701.5	63.0	484	9 US-10-005-921-2	Sequence 2, Appl
9	465	41.7	93	10 US-09-864-761-36370	Sequence 36370, A
10	248	22.3	182	10 US-09-410-194-24	Sequence 24, Appl
11	239	21.5	171	10 US-09-410-194-4	Sequence 4, Appl
12	234	21.0	169	10 US-09-410-194-2	Sequence 2, Appl
13	234	21.0	188	10 US-09-410-194-23	Sequence 23, Appl
14	198.5	17.8	64.0	10 US-09-410-194-5	Sequence 5, Appl
15	192.5	17.3	479	10 US-09-410-194-20	Sequence 20, Appl
16	185.5	16.7	177	10 US-09-410-194-7	Sequence 7, Appl
17	170.5	15.3	171	10 US-09-410-194-1	Sequence 1, Appl
18	170.5	15.3	171	10 US-09-410-194-13	Sequence 13, Appl
19	170.5	15.3	250	9 US-10-068-564-48	Sequence 48, Appl

#### ALIGNMENTS

RESULT 1  
 US-09-410-194-15  
 Patent No. US2002005030A1  
 GENERAL INFORMATION:  
 APPLICANT: Tschopp, Jurg  
 APPLICANT: Thome, Margot  
 APPLICANT: Burns, Kimberly  
 APPLICANT: Irmler, Marzen  
 APPLICANT: Hahne, Michael  
 APPLICANT: Schroter, Michael  
 APPLICANT: Schneider, Pascal  
 APPLICANT: Bodmer, Jean-Luc  
 APPLICANT: Steiner, Veronique  
 APPLICANT: Rimoldi, Donata  
 APPLICANT: Hofmann, Kay  
 APPLICANT: French, E. Lars  
 APPLICANT: INVENTION: FLIP GENES AND FLIP PROTEINS  
 FILE REFERENCE: 1114-002001  
 CURRENT APPLICATION NUMBER: US/09/410,194  
 CURRENT FILING DATE: 1999-09-30  
 PRIORITY APPLICATION NUMBER: PCV/EP98/01857  
 PRIORITY FILING DATE: 1998-03-31  
 PRIORITY APPLICATION NUMBER: GERMANY 197 13 393.2  
 PRIORITY FILING DATE: 1997-04-01  
 NUMBER OF SEQ ID NO'S: 27  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 15  
 LENGTH: 221  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-410-194-15

Query Match Similarity 100.0%; Score 1114; DB 10;  
 Best Local Similarity 100.0%; Pmid: 7.e-9;  
 Matches 221; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

OY 1 MSAEVTHQVEEALDTDEKEMLFLCRDAVIDVPPNVRDLIDLRLERGKLSYGDLAELLY 60  
 1 MSAEVTHQVEEADTDEKEMLFLCRDAVIDVPPNVRDLIDLRLERGKLSYGDLAELLY 60  
 Db 1 MSAEVTHQVEEADTDEKEMLFLCRDAVIDVPPNVRDLIDLRLERGKLSYGDLAELLY 60  
 Qy 61 RVRRFDLLKRILKMDRKAVETHLRLRNPHLVSDYRVLMAEIGEDLDKSDVSSLFLMKDM 120

RESULT 2  
 US-09-410-194-22  
 Sequence 22, Application US/09/410194  
 Patent No. US20020095030A1  
 GENERAL INFORMATION:  
 APPLICANT: Tschopp, Jurg  
 APPLICANT: Thome, Margot  
 APPLICANT: Burns, Kimberly  
 APPLICANT: Irmeler, Marten  
 APPLICANT: Hahne, Michael  
 APPLICANT: Schreiter, Michael  
 APPLICANT: Schneider, Pascal  
 APPLICANT: Bodmer, Jean-Luc  
 APPLICANT: Steiner, Veronique  
 APPLICANT: Rimoldi, Donata  
 APPLICANT: Hofmann, Kay  
 APPLICANT: French, E. Lars  
 TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS  
 FILE REFERENCE: 11141-002001  
 CURRENT APPLICATION NUMBER: US/09/410,194  
 CURRENT FILING DATE: 1999-09-30  
 PRIORITY APPLICATION NUMBER: PCT/EP98/01857  
 PRIOR FILING DATE: 1998-03-31  
 PRIORITY NUMBER: GERMANY 197 13 393.2  
 PRIORITY FILING DATE: 1997-04-01  
 NUMBER OF SEQ ID NOS: 27  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 22  
 LENGTH: 221  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-410-194-22

Query Match 100.0%; Score 1114; DB 10; Length 221;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-95;  
 Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAEVTHOYEALDTDEKMLFLCRDVAIDVPPNVRDLDLRLERGKLSVGDLAEELLY 60  
 DB 1 MSAEVTHOYEALDTDEKMLFLCRDVAIDVPPNVRDLDLRLERGKLSVGDLAEELLY 60

QY 61 RVRFEDLKRIKLMDRKAVETHLLRNPVLSDYRVLMAEIGEDLDKSDVSSLFLMKDM 120  
 DB 61 RVRFEDLKRIKLMDRKAVETHLLRNPVLSDYRVLMAEIGEDLDKSDVSSLFLMKDM 120

QY 121 GRKISKERSFLDLYVELEKLNLVAYPDQLLCLKNTHRIDLTKTQKYKSVQAGT 180  
 DB 121 GRKISKERSFLDLYVELEKLNLVAYPDQLLCLKNTHRIDLTKTQKYKSVQAGT 180

QY 121 GRKISKERSFLDLYVELEKLNLVAYPDQLLCLKNTHRIDLTKTQKYKSVQAGT 180  
 DB 121 GRKISKERSFLDLYVELEKLNLVAYPDQLLCLKNTHRIDLTKTQKYKSVQAGT 180

QY 181 SYRNVLQAATQKSLSKDPNNFRMITYAHCPDLKILGNCM 221  
 DB 181 SYRNVLQAATQKSLSKDPNNFRMITYAHCPDLKILGNCM 221

QY 181 SYRNVLQAATQKSLSKDPNNFRMITYAHCPDLKILGNCM 221  
 DB 181 SYRNVLQAATQKSLSKDPNNFRMITYAHCPDLKILGNCM 221

RESULT 3  
 US-09-861-270-2  
 Sequence 2, Application US/09/861270  
 Patent No. US20020052474A1  
 GENERAL INFORMATION:  
 APPLICANT: Sui, Hong-Bing  
 APPLICANT: Goeddel, David V.

RESULT 4  
 US-09-410-194-11  
 Sequence 11, Application US/09/10194  
 Patent No. US20020095030A1  
 GENERAL INFORMATION:  
 APPLICANT: Tschopp, Jurg  
 APPLICANT: Thome, Margot  
 APPLICANT: Burns, Kimberly  
 APPLICANT: Irmeler, Marten  
 APPLICANT: Hahne, Michael  
 APPLICANT: Schreiter, Michael  
 APPLICANT: Schneider, Pascal  
 APPLICANT: Bodmer, Jean-Luc  
 APPLICANT: Steiner, Veronique

; APPLICANT: Rimoldi, Donata  
 ; APPLICANT: Hofmann, Ray  
 ; APPLICANT: French, E. Lars  
 ; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS  
 ; FILE REFERENCE: 11411-002001  
 ; CURRENT APPLICATION NUMBER: US/09/410.194  
 ; CURRENT FILING DATE: 1999-09-30  
 ; PRIOR APPLICATION NUMBER: PCT/EP98/01857  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2  
 ; PRIOR FILING DATE: 1997-04-01  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 11  
 ; LENGTH: 480  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-410-194-11

Query Match 90.4%; Score 1007; DB 10; Length 480;  
 Best Local Similarity 99.5%; Pred. No. 1.4e-84;  
 Matches 202; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSAEVIHOVEALDTEDEKMLFLCRDVAIDVYPPNVRDLDLTLERGKLSVGDLAELLY 60  
 Db 1 MSAEVIHOVEALDTEDEKMLFLCRDVAIDVYPPNVRDLDLTLERGKLSVGDLAELLY 60

Qy 61 RVRRFDLKLRLKMRDKAVETHLLRNPFLHSYFVRLMAEGLDDKSVDSSLFLMKDM 120  
 Db 61 RVRRFDLKLRLKMRDKAVETHLLRNPFLHSYFVRLMAEGLDDKSVDSSLFLMKDM 120

Qy 121 GRGKISKEKSFLDVLELEKLNLVAPDQLDLLEKCLKNIHRIDLTKIQKYKSVQAGT 180  
 Db 121 GRGKISKEKSFLDVLELEKLNLVAPDQLDLLEKCLKNIHRIDLTKIQKYKSVQAGT 180

Qy 181 SYRNVLQAIAQSLKDPSSNNFRM 203  
 Db 181 SYRNVLQAIAQSLKDPSSNNFRM 203

RESULT 6  
 US-09-410-194-12

; Sequence 12, Application US/09410194  
 ; Patent No. US/2002/0095030A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tschopp, Jurg  
 ; APPLICANT: Thome, Margot  
 ; APPLICANT: Burns, Kimberly  
 ; APPLICANT: Irmier, Marten  
 ; APPLICANT: Hahne, Michael  
 ; APPLICANT: Schroter, Michael  
 ; APPLICANT: Schneider, Pascal  
 ; APPLICANT: Bodmer, Jean-Luc  
 ; APPLICANT: Steiner, Veronique  
 ; APPLICANT: Rimoldi, Donata  
 ; APPLICANT: Hofmann, Ray  
 ; APPLICANT: French, E. Lars  
 ; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS  
 ; FILE REFERENCE: 1141-002001  
 ; CURRENT FILING DATE: 1999-09-30  
 ; PRIOR APPLICATION NUMBER: US/09/410,194  
 ; CURRENT FILING DATE: 1999-09-30  
 ; PRIOR APPLICATION NUMBER: US/09/410,194  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SEQ ID NO: 12  
 ; LENGTH: 481  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-09-410-194-12

RESULT 5  
 US-09-410-194-17

; Sequence 17, Application US/09410194  
 ; Patent No. US/2002/0095030A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tschopp, Jurg  
 ; APPLICANT: Thome, Margot  
 ; APPLICANT: Burns, Kimberly  
 ; APPLICANT: Irmier, Marten  
 ; APPLICANT: Hahne, Michael  
 ; APPLICANT: Schroter, Michael  
 ; APPLICANT: Schneider, Pascal  
 ; APPLICANT: Bodmer, Jean-Luc  
 ; APPLICANT: Steiner, Veronique  
 ; APPLICANT: Rimoldi, Donata  
 ; APPLICANT: Hofmann, Ray  
 ; APPLICANT: French, E. Lars  
 ; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS  
 ; FILE REFERENCE: 11411-002001  
 ; CURRENT APPLICATION NUMBER: US/09/410.194  
 ; CURRENT FILING DATE: 1999-09-30  
 ; PRIOR APPLICATION NUMBER: PCT/EP98/01857  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2  
 ; PRIOR FILING DATE: 1997-04-01  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: FastSEQ for Windows Version 4.0

Query Match 64.0%; Score 713; DB 10; Length 481;  
 Best Local Similarity 74.5%; Pred. No. 1.3e-57;  
 Matches 146; Conservative 19; Mismatches 29; Indels 2; Gaps 2;

Qy 1 MSAEVIHOVEALDTEDEKMLFLCRDVAIDVYPPNVRDLDLTLERGKLSVGDLAELLY 60  
 Db 6 VSEAEVIHOVECLDEDKMLFLCRDVTENLAPNVRDLDLSERGQSFATLAEELLY 65

Qy 61 RVRRFDLKLRLKMRDKAVETHLLRNPFLHSYFVRLMAEGLDDKSVDSSLFLMKDM 120  
 Db 66 RVRRFDLKLRLKMRDKAVETHLLRNPFLHSYFVRLMIGESLDQNDYSLVFLTRDT 125

Qy 121 GRGKISKEKSFLDVLELEKLNLVAPDQLDLLEKCLKNIHRIDLTKIQKYKSVQAGT 180  
 Db 126 GRGKIAKOKSFLDVLELEKLNLJASDQLNLLEKCLKNIHRIDLNTKIQYTQSSQA-R 184

Qy 181 SYRNVLQAIAQSLK 195  
 Db 185 SNNNTLQASPLPKLSIK 200

US-09-410-194-17

RESULT 7  
US-09-410-194-19  
Sequence 19, Application US/09410194  
; Patent No. US20030095030A1  
; GENERAL INFORMATION:  
; APPLICANT: Tschopp, Jurg  
; APPLICANT: Burns, Kimberly  
; APPLICANT: Irmler, Marten  
; APPLICANT: Hanne, Michael  
; APPLICANT: Schroter, Michael  
; APPLICANT: Schneider, Pascal  
; APPLICANT: Bodmer, Jean-Luc  
; APPLICANT: Steiner, Veronique  
; APPLICANT: Rimoldi, Donata  
; APPLICANT: Hoffmann, Kay  
; APPLICANT: French, E. Lars  
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS  
; CURRENT APPLICATION NUMBER: US/09/10,194  
; CURRENT FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: PCT/EP98/01857  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2  
; PRIOR FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 481  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-410-194-19

Query Match 64.0%; Score 713; DB 10; Length 481;  
Best Local Similarity 74.5%; Pred. No. 1.3e-57;  
Matches 146; Conservative 19; Mismatches 29; Indels 2; Gaps 2;

Qy 1 MSAAVTHOYEALDTDEKMLFLCRDVAIDVPPNVDLRLERGKLSVGDLLAEYL 60  
Db 6 VSAEVTHOYECLDEDKEMMLFLCRDVTENLAAPVNVDLDSERQQLSFTLAELYL 65

Qy 61 RVRRFDLKLRLKMDRKAVETHLRLRPHLYSDYRVLMAEIGEDLDKSYSSLLFLMKDYM 120  
Db 66 RVRRFDLKLRLKTDKATEDHLRNPFLVSDYRVLMAEIGEDLDKSYSSLLFLTRRYT 125

Qy 121 GRGKISKERSFLDVLELKRLNLYAPDQDLLEKLNHRIIDLTKTQKYKOSVQGGT 180  
Db 126 GRGKIAKDSFLDVLELKLNLYASDQNLLEKLNHRIIDLTKTQKYTQSSQGR-R 184

Qy 181 SYRNYLQQAIQK-SLK 195  
Db 185 SNMNTLQASLPKLSIK 200

RESULT 8  
US-10-005-921-2  
Sequence 2, Application US/10005921  
; Patent No. US20020174450A1  
; GENERAL INFORMATION:  
; APPLICANT: Alien, Keith D.  
; APPLICANT: Leviten, Michael W.  
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CASH GENE  
; FILE REFERENCE: R-714  
; CURRENT APPLICATION NUMBER: US/10/005,921  
; CURRENT FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: US 60/254,902  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2

Query Match 63.0%; Score 701.5; DB 9; Length 484;  
Best Local Similarity 73.4%; Pred. No. 1.4e-56;  
Matches 146; Conservative 19; Mismatches 29; Indels 5; Gaps 3;

Qy 1 MSAAVTHOYEALDTDEKMLFLCRDVAIDVPPNVDLRLERGKLSVGDLLAEYL 60  
Db 6 VSAEVTHOYECLDEDKEMMLFLCRDVTENLAAPVNVDLDSERQQLSFTLAELYL 65

Qy 61 RVRRFDLKLRLKMDRKAVETHLRLRPHLYSDYRVLMAEIGEDLDKSYSSLLFLTRRYT 125

Qy 118 DYNGRGKISKERSFLDVLELKRLNLYAPDQDLLEKLNHRIIDLTKTQKYKOSVQGGT 177  
Db 126 DTGTRGKIAKDSFLDVLELKLNLYASDQNLLEKLNHRIIDLTKTQKYTQSSQG 185

RESULT 9  
US-09-864-761-3637/0  
; Sequence 36370, Application US/09864761  
; Patent No. US20020046763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Shannon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263,6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR APPLICATION NUMBER: US 60/254,902  
; PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO: 36370  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OPHER INFORMATION: MAP TO AC007272.2  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2  
OPHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1  
OPHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.9  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.5  
OTHER INFORMATION: EXPRESSED IN BT4/4, SIGNAL = 2.6  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2  
OTHER INFORMATION: SWISSPROT HIT: Q66674, EVALUATE 3.00e-04  
OPHER INFORMATION: EST\_HUMAN HIT: W22795.1, EVALUATE 2.000e-46

RESULT 11  
US-09-410-194-4

Query Match 41.7%; Score 465; DB 10; Length 93;  
Best Local Similarity 100.0%; Pred. No. 8.7e-36; Indels 0; Gaps 0;

Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSAEVHQVEEALDTDEKMLFLCRDVAIDVPPNVRDLIDLPERGKLISVGDAELLY 60  
Db 1 MSAEVHQVEEALDTDEKMLFLCRDVAIDVPPNVRDLIDLPERGKLISVGDAELLY 60

Qy 61 RYRFLDLKRLKMDRKAVETHLRLPHLVSDY 93  
Db 61 RYRFLDLKRLKMDRKAVETHLRLPHLVSDY 93

RESULT 10  
US-09-410-194-24

Query Match 22.3%; Score 248; DB 10; Length 171;  
Best Local Similarity 32.4%; Pred. No. 1e-14; Indels 65; Gaps 4;

Matches 56; Conservative 44; Mismatches 65; Indels 65; Gaps 4;

Qy 1 MSAEVHQVEEALDTDEKMLFLCRDVAIDVPPNVRDL--LDLIRERGKLISVGDAE 57  
Db 2 VTRDVLIAETHLNQNKEFTWFLD--PYPIKECKDFPLTENHHSKRKIRYPLIE 58

Qy 58 LYRVRFLDLKRLKMDRKAVETHLRLNP--HLYSDYRVLMAEIGEDLDKSPDSSLJFLM 116  
Db 59 LYIYLORFDLRSIFLDRVKDQITSSHVKYISPKQLFSGONIDDEDLISKFIS 118

Qy 117 KDMGRGKISKEKSFLDVLVELEKLNLYAPDOLLEKCLKNHRDLTKIQ 169  
Db 119 MNYIGRSP-SKIKNYLDWVRALEKVDMGPDNLDFETFKQIHRMDIVKMK 170

Software: FastSEQ for Windows Version 4.0  
SEQ ID NO: 24  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Bovine herpesvirus 4  
US-09-410-194-24

Query Match 22.3%; Score 248; DB 10; Length 182;  
Best Local Similarity 32.4%; Pred. No. 1.e-15;

RESULT 12  
US-09-410-194-2

; Sequence 2, Application US/09410194  
; Patent No. US20020095030A1  
; GENERAL INFORMATION:  
; APPLICANT: Tschopp, Jurg  
; APPLICANT: Burns, Kimberly  
; APPLICANT: Irmler, Marten  
; APPLICANT: Hahne, Michael  
; APPLICANT: Schröter, Michael  
; APPLICANT: Schneider, Pascal  
; APPLICANT: Bodmer, Jean-Luc  
; APPLICANT: Steiner, Veronique  
; APPLICANT: Rimoldi, Donata  
; APPLICANT: Hofmann, Kay  
; APPLICANT: French, E. Lars  
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS  
; FILE REFERENCE: 11141-002001  
; CURRENT APPLICATION NUMBER: US/09/410,194  
; CURRENT FILING DATE: 1999-09-30  
; PRIORITY APPLICATION NUMBER: PCT/EP98/01857  
; PRIORITY FILING DATE: 1998-03-31  
; PRIORITY APPLICATION NUMBER: GERMANY 197 13 393.2  
; PRIORITY FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 4  
; LENGTH: 171  
; TYPE: PRT  
; ORGANISM: Bovines herpesvirus 4  
; US-09-410-194-4

Query Match 21.5%; Score 239; DB 10; Length 171;  
Best Local Similarity 32.4%; Pred. No. 1e-14; Indels 65; Gaps 4;

Matches 56; Conservative 44; Mismatches 65; Indels 65; Gaps 4;

Qy 1 MSAEVHQVEEALDTDEKMLFLCRDVAIDVPPNVRDL--LDLIRERGKLISVGDAE 57  
Db 2 VTRDVLIAETHLNQNKEFTWFLD--PYPIKECKDFPLTENHHSKRKIRYPLIE 58

Qy 58 LYRVRFLDLKRLKMDRKAVETHLRLNP--HLYSDYRVLMAEIGEDLDKSPDSSLJFLM 116  
Db 59 LYIYLORFDLRSIFLDRVKDQITSSHVKYISPKQLFSGONIDDEDLISKFIS 118

Qy 117 KDMGRGKISKEKSFLDVLVELEKLNLYAPDOLLEKCLKNHRDLTKIQ 169  
Db 119 MNYIGRSP-SKIKNYLDWVRALEKVDMGPDNLDFETFKQIHRMDIVKMK 170

Software: FastSEQ for Windows Version 4.0  
SEQ ID NO: 24  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Bovine herpesvirus 4  
US-09-410-194-24

Query Match 22.3%; Score 248; DB 10; Length 182;  
Best Local Similarity 32.4%; Pred. No. 1.e-15;

RESULT 12  
US-09-410-194-2

; Sequence 2, Application US/09410194  
; Patent No. US20020095030A1  
; GENERAL INFORMATION:  
; APPLICANT: Tschopp, Jurg  
; APPLICANT: Burns, Kimberly  
; APPLICANT: Irmler, Marten  
; APPLICANT: Hahne, Michael  
; APPLICANT: Schröter, Michael  
; APPLICANT: Schneider, Pascal  
; APPLICANT: Bodmer, Jean-Luc  
; APPLICANT: Steiner, Veronique  
; APPLICANT: Rimoldi, Donata  
; APPLICANT: Hofmann, Kay  
; APPLICANT: French, E. Lars  
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS  
; FILE REFERENCE: 11141-002001  
; CURRENT APPLICATION NUMBER: US/09/410,194  
; CURRENT FILING DATE: 1999-09-30  
; PRIORITY APPLICATION NUMBER: PCT/EP98/01857  
; PRIORITY FILING DATE: 1998-03-31  
; PRIORITY APPLICATION NUMBER: GERMANY 197 13 393.2  
; PRIORITY FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 4  
; LENGTH: 171  
; TYPE: PRT  
; ORGANISM: Bovines herpesvirus 4  
; US-09-410-194-4

RESULT 13  
 US-09-410-194-23  
 ; Sequence 23, Application US/09410194  
 ; Patent No. US20020095030A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Irmller, Marten  
 ; APPLICANT: Hahne, Michael  
 ; APPLICANT: Schreiter, Pascal  
 ; APPLICANT: Schneider, Jean-Luc  
 ; APPLICANT: Bodmer, Jean-Luc  
 ; APPLICANT: Steiner, Veronique  
 ; APPLICANT: Rimaldi, Donata  
 ; APPLICANT: Hofmann, Kay  
 ; APPLICANT: French, E. Lars  
 ; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS  
 ; FILE REFERENCE: 11141-002001  
 ; CURRENT APPLICATION NUMBER: US/09/410,194  
 ; CURRENT FILING DATE: 1999-09-30  
 ; PRIORITY APPLICATION NUMBER: PCT/EP98/01857  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: DE 197 13 393.2  
 ; PRIOR FILING DATE: 1997-04-01  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 169  
 ; TYPE: PRT  
 ; ORGANISM: Humanes herpesvirus 8  
 US-09-410-194-2

Query Match 21.0%; Score 234; DB 10; Length 169;  
 Best Local Similarity 34.3%; Pred. No. 2.9e-14;  
 Matches 55; Conservative 39; Mismatches 64; Indels 8; Gaps 3;

Qy 4 EVIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLDILR---ERGKLSVGDLAELLY 60  
 Db 5 EVLCEVARLKLTGTDREVVFL--LNVPFQPTLAQLGALARKEGRLLPFLAECLF 61

Qy 61 RVRFDLKLRLKMDRKAVETHLLRNPHVSYRVLMAEIGEDLDKSVDSSLFMLKDM 120  
 Db 62 RAGRDLRDLHDPFLERHLLAGTMSYFSPIQTVLHVDGECARDIRSLFLSKDTI 121

Qy 121 GRGKLSKEFSFLDVLELEKLNVLAPDOLLEKLNKLNHRIDLTKTQ 169  
 Db 122 -GSRSTPQTFLHVVYCMEMLDQPTDVAJMSMLRSLSRVDLQRQVQ 168

RESULT 14  
 US-09-410-194-5  
 ; Sequence 5, Application US/09410194  
 ; Patent No. US20020095030A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tschoopp, Jurg  
 ; APPLICANT: Thomé, Margot  
 ; APPLICANT: Burns, Kimberly  
 ; APPLICANT: Irmller, Marten  
 ; APPLICANT: Hahne, Michael  
 ; APPLICANT: Schreiter, Michael  
 ; APPLICANT: Schneider, Pascal  
 ; APPLICANT: Bodmer, Jean-Luc  
 ; APPLICANT: Steiner, Veronique  
 ; APPLICANT: Rimoldi, Donata  
 ; APPLICANT: Hofmann, Kay  
 ; APPLICANT: French, E. Lars  
 ; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS  
 ; CURRENT APPLICATION NUMBER: US/09/410,194  
 ; CURRENT FILING DATE: 1999-09-30  
 ; PRIOR APPLICATION NUMBER: PCT/EP98/01857  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: DE 197 13 393.2  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 5  
 ; LENGTH: 169  
 ; TYPE: PRT  
 ; ORGANISM: Molluscum contagiosum virus subtype 1  
 US-09-410-194-5

Query Match 17.8%; Score 198.5; DB 10; Length 169;  
 Best Local Similarity 31.5%; Pred. No. 5.2e-11;  
 Matches 54; Conservative 35; Mismatches 63; Indels 9; Gaps 6;

Qy 7 HQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLDILRERGKLSVGDLAELLYRVRFRD 66  
 Db 9 HLLE-LDSHEDSLLFLCHDAFGCT-TVTOALCSUSQRKLTAALEVNLVLRMD 65

Qy 67 LLKRILKMDRKAVETHLLRNPHVSYRVLMAEIGEDLDKSVDSS-IFL--MKDYMGRC 123  
 Db 66 LLKSRFGLSKEGAQ--LIGTSFTRYKLMVCGEELDSSERLRFACNUPSUSTA 123

Qy 124 KISKEKSFLDLVLELEKLNVLAPDOLLEKLNKLNHRIDL 164  
 Db 124 -LSSSRFWELVLALENGLVSPSSVSLADMRLTRRLDL 163

RESULT 15  
 US-09-410-194-20  
 ; Sequence 20, Application US/09410194  
 ; Patent No. US20020095030A1

```

; GENERAL INFORMATION:
; APPLICANT: Tschopp, Jurg
; APPLICANT: Thome, Margot
; APPLICANT: Burns, Kimberly
; APPLICANT: Irmiger, Marten
; APPLICANT: Hahne, Michael
; APPLICANT: Schrötter, Michael
; APPLICANT: Schneider, Pascal
; APPLICANT: Bodmer, Jean-Luc
; APPLICANT: Steiner, Veronique
; APPLICANT: Rimoldi, Donata
; APPLICANT: Hofmann, Kay
; APPLICANT: French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410,194
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 20
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-104-20

Query Match 17.38; Score 192.5; DB 10; Length 479;
Best Local Similarity 26.8%; Pred. No. 6.9e-10;
Matches 53; Conservative 56; Mismatches 64; Indels 25; Gaps 8;

Qy 6 INNOVEALDTDEKMLFLCRRDVAIDVPPN---VRDLI--LDRERGLSVDGLA-- 56
Db 7 LYDGEQIDSLEDASLASKFL---SLDYIPQRKQEPIKDALMFLQRQKMLEESENLSFL 62
Qy 57 -ELLYRYRFLKLRIKMDRKAVETHLRLNP--HLVSDYRVLMAIGEDLDKSVDSSLI 113
Db 63 KELLFRNRLDILITINTRKEMERE LQPGRQISATRVMLTQISEEVSRSEERSFK 121
Qy 114 FLMKDYGNGRKISKEKSFLIVYELEKLNLYAPDQLDLEKCLKNIHRIDLTKIQKYQ 173
Db 122 FLLQEETSRCKLDDMMNLDTIEMERKVLGEKLDILKRVCAQINKSLLK1-INDYEE 180
Qy 174 -----SVQGAGTSYRN 184
Db 181 FSKERSSSLEGSPDEFN 198

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Search completed: April 12, 2003, 22:40:51  
 Job time : 11.772 secs

GenCore version 5.1.4\_p5\_4578  
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## OM protein - protein search, using sw model

Run on: April 12, 2003, 20:50:13 ; Search time 9.14265 Seconds

(without alignments)  
711.223 Million cell updates/sec

Title: US-09-380-546A-4

Perfect score: 11.4

Sequence: 1 MSAEVTHQEERBALDTDEKEM..... RMITPYAHCDLKLIGNCNM 221

Scoring table: BL2SUM62

Gapop 10.0 , Gapext 0.5

Searched: 265574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA;\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep: \*  
2: /con2\_6/ptodata/1/1aa/5B\_COMB.pep: \*  
3: /con2\_6/ptodata/1/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep: \*  
5: /con2\_6/ptodata/1/1aa/BCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1114	100.0	221	4	US-09-382-155-17
2	1114	100.0	221	4	US-09-074-044A-17
3	1015	91.1	445	3	US-09-859-167-2
4	1015	91.1	445	3	US-09-109-273-2
5	1015	91.1	445	4	US-09-276-993-2
6	1007	90.4	480	4	US-09-795-088A-2
7	987	88.6	480	4	US-09-069-023-34
8	417	37.4	84	4	US-09-074-044A-2
9	403	36.2	84	4	US-09-382-155-2
10	384	34.5	78	4	US-09-382-155-2
11	384	34.5	78	4	US-09-074-044A-1
12	218.5	19.6	741	4	US-09-382-155-21
13	218.5	19.6	241	4	US-09-074-044A-21
14	195	17.5	220	2	US-08-807-200-2
15	195	17.5	220	4	US-09-001-777-2
16	192.5	17.3	235	4	US-08-983-502-5
17	192.5	17.3	235	5	PCT-US96-10521-5
18	192.5	17.3	257	1	US-08-618-164-2
19	192.5	17.3	277	4	US-08-983-502-8
20	192.5	17.3	479	2	PCT-US96-10521-8
192.5	17.3	479	3	US-08-852-782-3	
192.5	17.3	479	4	US-09-001-777-12	
192.5	17.3	479	5	PCT-US96-10521-7	
192.5	17.3	479	5	US-08-983-502-7	
192.5	17.3	479	6	US-08-983-502-25	
192.5	17.3	479	7	PCT-US96-10521-25	
192.5	17.3	479	8	US-09-227-721-27	

## ALIGNMENTS

RESULT 1  
US-09-382-155-17  
; Sequence 17, Application US/09382155B  
; Patent No. 6160095  
; GENERAL INFORMATION:  
; APPLICANT: CHAUDHARY, PREET M  
; INVENTOR: HOOD, LEROY  
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS  
; PATHWAYS AND METHODS OF USING THE SAME  
; FILE REFERENCE: Chaudhary  
; CURRENT APPLICATION NUMBER: US/09/382,155B  
; CURRENT FILING DATE: 1999-08-24  
; EARLIER APPLICATION NUMBER: 09/074, 044  
; EARLIER FILING DATE: 1998-05-07  
; NUMBER OF SEQ ID NO: 40  
; SEQ ID NO 17  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-382-155-17

Query Match Score 100.0% ; Score 1114; DB 4; Length 221;  
Best Local Similarity 100.0%; Pred. No. 6. 8e-105; Mismatches 0; Indels 0; Gaps 0;  
Matches 221; Conservative 0;

Qy	1	MSAEVTHQEERBALDTDEKEMIIFLCRQDAVIDVPPNVRDLDILRLERGKLSVGDLAELLY 60
Db	1	MSEREVTHQEERBALDTDEKEMIIFLCRQDAVIDVPPNVRDLDILRLERGKLSVGDLAELLY 60
Qy	61	RYRFDLIKRILKMDRKAVETHLLRNPFLYSDRVYLMAEIGEDLKSDVSSLIFLMKDM 120
Db	61	RYRFDLIKRILKMDRKAVETHLLRNPFLYSDRVYLMAEIGEDLKSDVSSLIFLMKDM 120
Qy	121	GRKSKRSKEFSLDLVVELEKLNVLAPDOLDLLEKRNTHIDLTKIQKYQSVOGAGT 180
Db	121	GRKSKRSKEFSLDLVVELEKLNVLAPDOLDLLEKCNHIDLTKIQKYQSVOGAGT 180
Qy	181	SYRNVLQIAOKSLKDPSNNFRMITYAHCPDKLKGNCNM 221
Db	181	STRNVLQIAOKSLKDPSNNFRMITYAHCPDKLKGNCNM 221

RESULT 2  
US-09-074-044A-17  
; Sequence 17, Application US/09074044A  
; Patent No. 620458  
; GENERAL INFORMATION:  
; APPLICANT: CHAUDHARY, PREET M  
; APPLICANT: HOOD, LEROY

Sun Apr 13 14:24:22 2003

TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB,JNK AND APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME  
 NUMBER OF SEQUENCES: 28  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS  
 STREET: 2415 GRAND BLVD., SUITE 400  
 CITY: KANSAS CITY  
 STATE: MISSOURI  
 COUNTRY: USA  
 ZIP: 64108

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/074.044A  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: COLLINS, JOHN M.  
 REGISTRATION NUMBER: 26,262  
 REFERENCE/DOCKET NUMBER: 26588  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 816/474-9050  
 TELEFAX: 816/474-9057

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 221 amino acids  
 TYPE: amino acid

STRANDEDNESS:  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: protein

ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens

US-09-074.044A-17

Query Match 100.0%; Score 1114; DB 4; Length 221;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-105; Gaps 0;  
 Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSAEVTHQEALDDEKEMLLFLCRDVAIDVYPNVNRDLDLIRERGKLSVGDAELLY 60  
 Db 1 MSAEVTHQEALDDEKEMLLFLCRDVAIDVYPNVNRDLDLIRERGKLSVGDAELLY 60

Qy 61 RVRRFDLKLRLKMRDKAVETHLLRNPHLVSDYRVLMAEIGEDLKSDVSSLFLMKDM 120  
 Db 61 RVRRFDLKLRLKMRDKAVETHLLRNPHLVSDYRVLMAEIGEDLKSDVSSLFLMKDM 120

Qy 61 RVRRFDLKLRLKMRDKAVETHLLRNPHLVSDYRVLMAEIGEDLKSDVSSLFLMKDM 120  
 Db 61 RVRRFDLKLRLKMRDKAVETHLLRNPHLVSDYRVLMAEIGEDLKSDVSSLFLMKDM 120

Qy 121 GRGKSKESKFLDVLVELEKLNVAPDQLLEKLNTHRIDLTKIQKYKOSVQAGT 180  
 Db 121 GRGKSKESKFLDVLVELEKLNVAPDQLLEKLNTHRIDLTKIQKYKOSVQAGT 180

Qy 181 SYRNVLQAIAOKSLKDPSNNFRMTPYAHCPDLKLGNC 221  
 Db 181 SYRNVLQAIAOKSLKDPSNNFRMTPYAHCPDLKLGNC 221

RESULT 3  
 US-08-859-167-2  
 ; Sequence 2, Application US/08859167  
 ; Patent No. 6037461  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alnemri, Emad S.  
 ; APPLICANT: Fernandez-Alnemri, Teresa  
 ; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF  
 ; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS  
 ; TITLE OF INVENTION: OF MAKING THE SAME  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461ris  
 ; STREET: One Liberty Place, 46th floor  
 ; CITY: Philadelphia

RESULT 3  
 US-08-859-167-2  
 ; Sequence 2, Application US/08859167  
 ; Patent No. 6037461  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alnemri, Emad S.  
 ; APPLICANT: Fernandez-Alnemri, Teresa  
 ; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF  
 ; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS  
 ; TITLE OF INVENTION: OF MAKING THE SAME  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461ris  
 ; STREET: One Liberty Place, 46th floor  
 ; CITY: Philadelphia

STATE: PA  
 COUNTRY: USA  
 ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: WINDOWS  
 SOFTWARE: WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/859.167  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DeLuca, Mark  
 REGISTRATION/DOCKET NUMBER: 33,229  
 REFERENCE/DOCUMENTATION INFORMATION:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-3100  
 TELEFAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 445 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-859-167-2

Query Match 91.1%; Score 1015; DB 3; Length 445;  
 Best Local Similarity 94.5%; Pred. No. 1.8e-94;  
 Matches 207; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MSAEVTHQEALDDEKEMLLFLCRDVAIDVYPNVNRDLDLIRERGKLSVGDAELLY 60  
 Db 1 MSAEVTHQEALDDEKEMLLFLCRDVAIDVYPNVNRDLDLIRERGKLSVGDAELLY 60

Qy 61 RVRRFDLKLRLKMRDKAVETHLLRNPHLVSDYRVLMAEIGEDLKSDVSSLFLMKDM 120  
 Db 61 RVRRFDLKLRLKMRDKAVETHLLRNPHLVSDYRVLMAEIGEDLKSDVSSLFLMKDM 120

RESULT 4  
 US-09-109-273-2  
 ; Sequence 2, Application US/09109273  
 ; Patent No. 6063760  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alnemri, Emad S.,  
 ; APPLICANT: Fernandez-Alnemri, Teresa  
 ; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF  
 ; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS  
 ; TITLE OF INVENTION: OF MAKING THE SAME  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760ris  
 ; STREET: One Liberty Place, 46th floor  
 ; CITY: Philadelphia

FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION NUMBER: 08/859,167  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Deluca, Mark  
 REGISTRATION NUMBER: 33,229  
 REFERENCE/DOCKET NUMBER: TJu-TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-3100  
 TELEFAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 445 amino acids  
 TOPOLGY: linear  
 MOLECULE TYPE: protein  
 US-09-109-273-2

Query Match 91.1%; Score 1015; DB 3; Length 445;  
 Best Local Similarity 94.5%; Pred No. 1.8e-94;  
 Matches 207; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MSAEVTHQEAEALDTDEKMLFLCRDVAIDVPPNVRDLDLIRERGKLSVGDLAELLY 60  
 Db 1 MSAEVTHQEAEALDTDEKMLFLCRDVAIDVPPNVRDLDLIRERGKLSVGDLAELLY 60

Qy 61 RVRRFDLLKRILMKDRKAVETHLLRNPRLVSDYRVLMAEIGEDLKSDSLIFLMKDYM 120  
 Db 61 RVRRFDLLKRILMKDRKAVETHLLRNPRLVSDYRVLMAEIGEDLKSDSLIFLMKDYM 120

Qy 121 GRGKISKEKSFSDLIVVELEKLNLVAPDQLDLERKLNHIDLTKTQKYKOSVOGAGT 180  
 Db 121 GRGKISKEKSFSDLIVVELEKLNLVAPDQLDLERKLNHIDLTKTQKYKOSVOGAGT 180

Qy 181 SYRNVLQAIIQSKLDPNSNFRMITYAHCPDLKLGNC 219  
 Db 181 SYRNVLQAIIQSKLDPNSNFRSPEERYKMKSKPLGIC 219

RESULT 5  
 US-09-276-993-2  
 ; Sequence 2, Application US/09276993  
 ; GENERAL INFORMATION:  
 APPLICANT: Alnemri, Enad S.  
 APPLICANT: Fernandez-Alnemri, Teresa  
 TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF  
 TITLE INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS  
 TITLE OF INVENTION: OF MAKING THE SAME  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & NO. 620780iris  
 STREET: One Liberty Place, 46th floor  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: WINDOWS  
 SOFTWARE: WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/276.993  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/859,167  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229  
 REFERENCE/DOCKET NUMBER: TJu-TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-3100  
 TELEFAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 445 amino acids  
 TOPOLGY: linear  
 MOLECULE TYPE: protein  
 US-09-276-993-2

Query Match 91.1%; Score 1015; DB 4; Length 445;  
 Best Local Similarity 94.5%; Pred No. 1.8e-94;  
 Matches 207; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MSAEVTHQEAEALDTDEKMLFLCRDVAIDVPPNVRDLDLIRERGKLSVGDLAELLY 60  
 Db 1 MSAEVTHQEAEALDTDEKMLFLCRDVAIDVPPNVRDLDLIRERGKLSVGDLAELLY 60

Qy 61 RVRRFDLLKRILMKDRKAVETHLLRNPRLVSDYRVLMAEIGEDLKSDSLIFLMKDYM 120  
 Db 61 RVRRFDLLKRILMKDRKAVETHLLRNPRLVSDYRVLMAEIGEDLKSDSLIFLMKDYM 120

Qy 121 GRGKISKEKSFSDLIVVELEKLNLVAPDQLDLERKLNHIDLTKTQKYKOSVOGAGT 180  
 Db 121 GRGKISKEKSFSDLIVVELEKLNLVAPDQLDLERKLNHIDLTKTQKYKOSVOGAGT 180

Qy 181 SYRNVLQAIIQSKLDPNSNFRMITYAHCPDLKLGNC 219  
 Db 181 SYRNVLQAIIQSKLDPNSNFRSPEERYKMKSKPLGIC 219

RESULT 6  
 US-08-795-088A-2  
 ; Sequence 2, Application US/08795088A  
 ; Patent No. 6242569  
 ; GENERAL INFORMATION:  
 APPLICANT: Sui, Hong-Bing  
 APPLICANT: Goedde, David V.  
 TITLE OF INVENTION: Regulators of Apoptosis  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Science & Technology Law Group  
 STREET: 75 Denlise Drive  
 CITY: Hillsborough  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94010  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/795,088A  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Osman, Richard A.  
 REGISTRATION NUMBER: 36,527  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 343-4341  
 TELEFAX: (650) 343-4342  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 480 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLGY: not relevant  
 MOLECULE TYPE: peptide

RESULT 7  
 US-09-069-023-34  
 ; Sequence 34, Application US/09069023A  
 ; Patent No. 6348573  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nunez, Gabriel  
 ; INOHARA, Naohiro  
 ; APPLICANT: Inohara, Naohiro  
 ; APPLICANT: Koseki, Takeyoshi  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
 ; SIGNALING PATHWAY INHIBITORS AND ACTIVATORS  
 ; FILE REFERENCE: UM-0333  
 ; CURRENT FILING DATE: 1998-04-27  
 ; NUMBER OF SEQ ID NOS: 38  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 34  
 ; LENGTH: 480  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-069-023-34

Query Match            90.4%; Score 1007; DB 4; Length 480;  
 Best Local Similarity 99.5%; Pred. No. 1.3e-93; 1; Mismatches 0; Indels 0; Gaps 0;  
 Matches 202; Conservative 1;

Qy        1 MSAEVTHQEPEALDDEKEMILFLCRDVAIDVPPNVRDLDLIRERGKLSVGDLAELLY 60  
 Db        1 MSAEVTHQEPEALDDEKEMILFLCRDVAIDVPPNVRDLDLIRERGKLSVGDLAELLY 60  
 Qy        61 RVRRFDLKLRLKMDRKAVETHLLRNPHLVSYRVLMAEGIDLKSDVSSLIFLMKDYM 120  
 Db        61 RVRRFDLKLRLKMDRKAVETHLLRNPHLVSYRVLMAEGIDLKSDVSSLIFLMKDYM 120  
 Qy        121 GRGKISKEKSFSDLVYVEKLNLVAPDQDLLECKLNTHRIDLTKIQKYKOSVOGAGT 180  
 Db        121 GRGKISKEKSFSDLVYVEKLNLVAPDQDLLECKLNTHRIDLTKIQKYKOSVOGAGT 180  
 Qy        181 SYRNLQAAIQSLKDPSSNFRM 203  
 Db        181 SYRNLQAAIQSLKDPSSNFRM 203

RESULT 8  
 US-09-074-044A-2  
 ; Sequence 2, Application US/09074044A  
 ; Patent No. 6207458  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHAUDHARY, PREET M  
 ; APPLICANT: HOOD, LEROY  
 ; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-kB, JNK AND APOPTOSIS

Query Match            90.4%; Score 1007; DB 4; Length 480;  
 Best Local Similarity 99.5%; Pred. No. 1.3e-93; 1; Mismatches 0; Indels 0; Gaps 0;  
 Matches 202; Conservative 1;

Qy        1 MSAEVTHQEPEALDDEKEMILFLCRDVAIDVPPNVRDLDLIRERGKLSVGDLAELLY 60  
 Db        1 MSAEVTHQEPEALDDEKEMILFLCRDVAIDVPPNVRDLDLIRERGKLSVGDLAELLY 60  
 Qy        61 RVRRFDLKLRLKMDRKAVETHLLRNPHLVSYRVLMAEGIDLKSDVSSLIFLMKDYM 120  
 Db        61 RVRRFDLKLRLKMDRKAVETHLLRNPHLVSYRVLMAEGIDLKSDVSSLIFLMKDYM 120  
 Qy        121 GRGKISKEKSFSDLVYVEKLNLVAPDQDLLECKLNTHRIDLTKIQKYKOSVOGAGT 180  
 Db        121 GRGKISKEKSFSDLVYVEKLNLVAPDQDLLECKLNTHRIDLTKIQKYKOSVOGAGT 180  
 Qy        181 SYRNLQAAIQSLKDPSSNFRM 203  
 Db        181 SYRNLQAAIQSLKDPSSNFRM 203

RESULT 9  
 US-09-382-155-2  
 ; Sequence 2, Application US/09382155B  
 ; Patent No. 6160095  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHAUDHARY, PREET M  
 ; APPLICANT: HOOD, LEROY  
 ; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-kB, JNK AND APOPTOSIS  
 ; FILE REFERENCE: Chaudhary  
 ; CURRENT APPLICATION NUMBER: US/09/382,155B  
 ; CURRENT FILING DATE: 1999-08-24  
 ; EARLIER APPLICATION NUMBER: 09/074,044  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SEQ ID NO 2  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; LENGTH: 84  
 ; TYPE: PRT  
 ; ORGANISM: HUMAN HERPESVIRUS 8  
 ; US-09-382-155-2

Query Match            36.2%; Score 403; DB 4; Length 84;

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Best Local Similarity 97.6%; Pred. No. 1.2e-33; Matches 82; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 90 VSDYRVLMAEIGELDKSDVSSLFLMKDNGRGKISKEKSFLDLVLELKLNLYAPDQL 149
Db 1 VSDYRVLMAEIGELDKSDVSSLFLMKDNGRGKISLESFLDLVLELKLNLYAPDQL 60
Qy 150 DLLEKCLKNTHRIDLTKTQIQQYQ 173
Db 61 DLLEKCLKNTHRIDLTKTQIQQYQ 84

RESULT 10
US-09-382-155-1
Sequence 1, Application US/09382155B
Patent No. 6160095
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
FILE REFERENCE: Chaudhary
CURRENT APPLICATION NUMBER: US/09/382,155B
CURRENT FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 09/074,044
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 78
TYPE: PRT
ORGANISM: Homo sapiens
US-09-382-155-1

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ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 26588
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: not relevant
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-074-04A-1

Query Match Score 34.5%; DB 4; Length 78;
Best Local Similarity 100.0%; Pred. No. 9e-32; Gaps 0;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSAEVIIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLDILRERGKLSVGDLAELLY 60
Db 1 MSAEVIIHQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLDILRERGKLSVGDLAELLY 60

Qy 61 RVRRFDLKLKRLKMDRKA 78
Db 61 RVRRFDLKLKRLKMDRKA 78

RESULT 12
US-09-382-155-21
Sequence 21, Application US/09382155B
Patent No. 6160095
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
APPLICANT: HOOD, LEROY
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF- $\kappa$ B, JNK AND APOPTOSIS
FILE REFERENCE: PATHWAYS AND METHODS OF USING THE SAME
CURRENT APPLICATION NUMBER: US/09/382-155B
CURRENT FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 09/074, 044
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 21
LENGTH: 241
TYPE: PRT
ORGANISM: Molluscum contagiosum virus
US-09-382-155-21

Query Match Score 19.6%; DB 4; Length 241;
Best Local Similarity 29.9%; Pred. No. 2.2e-14; Gaps 7;
Matches 64; Conservative 41; Mismatches 80; Indels 29; Gaps 7;

Qy 7 HQVEEALDTDEKEMLLFLCRDVAIDVPPNVRDLDILRERGKLSVGDLAELLYRVRRFD 66
Db 15 HLLEE-LDSDHESLJLFLCHDRAGPGCT-TVTOAQLSLSQRKLTLAAVEMLYVLRQMD 71
Qy 67 LLKRLLKMDRAVEFHLLRNHLPSDYRVLMAEGBDKSDVSSL-IFL-MKDQMGRC 123
Db 72 LIKSRSRGLSKRGAEQ-LLGTSFLPTRYKLMVCVGEELDSSELRLRFACNLNPSLSTA 129
Qy 124 KISKEKSFSDLIYVELEKLNLYAPDOLDLLEKCKLNTHRIDLTKIOKYKOSVQ----- 176
Db 130 -LSESSRFVELVLAENVLGVPSSVSLADMLRTLRLDCQOLVVEEOEQARYRYC 188
Db 177 -----GAGTSYRNVLQAIIQSKDP 197
Db 189 KASPSPLPVRTLRRHGASEHEOLCAMPVOEDSSD 222

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**RESULT 13**  
US-09-04-04A-21  
Sequence 21; Application US/09074044A  
; Patent No. 6207458  
; GENERAL INFORMATION:  
; APPLICANT: CHAUDIARY, PREET M  
; ADDRESS: HOOD, LEROV  
; TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; STREET: 2405 GRAND BLVD., SUITE 400  
; CITY: KANSAS CITY  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 64108  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/074 . 044A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COLLINS, JOHN M  
; REGISTRATION NUMBER: 26 , 262  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 816/474-9050  
; TELEFAX: 816/474-9057  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; STANDINGNESS:  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: MOLLUSCUM CONTAGIOSUM VIRUS

**US-09-04-04A-21**

Query Match 19 6%; Score 218 5; DB 4; Length 241;  
Best Local Similarity 29 9%; Pred. No. 2.2e-14;  
Matches 64; Conservative 41; Mismatches 80; Indels 29; Gaps 7;

Qy 7 HOVEEALDTDEKEMLFLCRDVAIDVPPNVRDLDLILRRGKLSVGDIELLYVRRRD 66  
Db 15 HLLER-LDSEDSLFLCHDAAPGCT-TYTOAICSLSOQRKUTLAALVEMYYVLQRD 71

Qy 67 LLKRLLKMDRKAVETHLLRNPHLVSDYRVLMAEIGDLKSDVSSL-IEFL--MHDYMGG 123  
Db 72 LKKSRREGLKSEGAEQ -LGTSFLTRYRKLIVCNGEELSSSELRLAFACNLPSLSTA 129

Qy 124 KISKEKSFIDLVVLEKLNUVAPDQLDLKLEKCLKNIHRIDLKTKIQKYKOSVO----- 176  
Db 130 -LSESSRFVELVLALENGLVSPSSVSVLADMRLTRRLDCQOLVEYEQEQQARYRYCY 188

Qy 177 -----GAGTSTRNVLQAIQKSLKD 197  
Db 189 AASPLSPVRLPRTLRRGHSASEHEQLCMVQESSDSP 222

**RESULT 14**  
US-08-007-200-2  
Sequence 2; Application US/08807200  
; Patent No. 5837837  
; GENERAL INFORMATION:  
; APPLICANT: Hunter, John J.  
; ADDRESS: Fish & Richardson P.C.

**RESULT 13**  
US-09-04-04A-21  
Sequence 21; Application US/09074044A  
; Patent No. 6207458  
; GENERAL INFORMATION:  
; APPLICANT: Shyjan, Andrew W.  
; ADDRESS: Wong, Grace H.W.  
; TITLE OF INVENTION: NOVEL FORMS OF CASPASE-8 AND  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FASTSEQ FOR Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/807,200  
; FILING DATE: 27-FEB-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07 334/021001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEX: 617-542-8906  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 220 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-807-200-2

Query Match 17 5%; Score 195; DB 2; Length 220;  
Best Local Similarity 27.6%; Pred. No. 4.6e-12;  
Matches 54; Conservative 54; Mismatches 70; Indels 18; Gaps 7;

Qy 6 IHOVEEALDTDEKEMLFLCRDVAIDVPPN----VRDLDI---LRLERGKLSVGDLA-- 56  
Db 7 LDYDGEOLDSEDLASLKF---SLDYLPQRKQEPKIDALMFLQRQKRMLESNLNFL 62

Qy 57 -ELLYVVRREPDLLKRLLKMDRKAVETHLLRNPL-HLVDYRVLMAEIGDLKSDVSSLI 113  
Db 63 KELLFRINRUDLITYLNTRKEEMRE-LQTPGRQAISAYRVMLYQISEEVSRSELRSKF 121

Qy 114 FLMKDMGRKGKISKESFLDLYVLEKLNUVAPDQLDLKLEKCLKNIHRIDLKTKIQKYKO 173  
Db 122 FLQOEISCKLDDMNLLDIFEMKRVILGEKGKDLIKRVCAQINKSLKI-INDYEE 180

Qy 174 SVQAGTTSRNVLQAA 189  
Db 181 FSKDFEGOSLPNEKOTS 196

**RESULT 15**  
US-09-001-777-2  
Sequence 2; Application US/09001777  
; Patent No. 6172190  
; GENERAL INFORMATION:  
; APPLICANT: Hunter, John J.  
; ADDRESS: Shyjan, Andrew W.  
; TITLE OF INVENTION: NOVEL FORMS OF CASPASE-8 AND USES THEREOF  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FASTSEQ FOR Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/807,200  
; FILING DATE: 27-FEB-1997

STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM Compatible  
 MEDIUM TYPE: Diskette  
 OPERATING SYSTEM: Windows 95  
 SOFTWARE: FASTSEQ for Windows Version 2.0b  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/001,777  
 FILING DATE: 31-DEC-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/807,200  
 FILING DATE: 27-FEB-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Freeman, John W.  
 REGISTRATION NUMBER: 29,066  
 REFERENCE/DOCKET NUMBER: 07334/021002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 220 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-09-001-777-2

Query Match 17.5%; Score 195; DB 4; Length 220;

Best Local Similarity 27.6%; Pred. No. 4.6e-12;  
 Matches 54; Conservative 54; Mismatches 70; Indels 18; Gaps 7;

Qy 6 IHOVEBALDTDEKEMLLFLCRDVAIDVPPN---VRDLIDI---LREQKLSVGDLA-- 56  
 Db 7 LYDIGSQLDEEDSLASKFL ---SIDIYIPQKQPIKDAIMLFORQERMLPEESNLSQL 62  
 Qy 57 -ELLYRVRFRDLLKRILKMDRAVETHLLRNP--HLYSDYRVLMAEIGEDDKSDVSSJ 113  
 Db 63 KELLPRINRIDLITYLNTRKEEMERE-LQTPGRAQISAYRMVLYQISEEVSRSELRSFK 121  
 Qy 114 FLMKDUMGRGKISKEKSFLDVLVVELEKNUVAPOLDLIEKCLNIHRDLKTKIQYKQ 173  
 Db 122 FLLQBEISKCKLDDMMNLDFIEMEKRVILGECKLDILKRVCAQINKSLLKI-INDYEE 180  
 Qy 174 SVQGACTSYRNVLQAA 189  
 Db 181 FSKDFGQSLPNERKOTS 196

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 Job time : 10.1427 secs

GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2003, 20:46:38 ; Search time 84.2937 Seconds  
(without alignments)  
14287.562 Million cell updates/sec

Title: US-09-380-546A-3  
Perfect score: 1373  
Sequence: 1 ggacgtcgaggcattacaat.....aaaaaaaaaaaaaaa 1373

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:  
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 2: /cgn2\_6/pktodata/2/pubpna/pct\_new\_pub.seq:  
 3: /cgn2\_6/pktodata/2/pubpna/us06\_new\_pub.seq:  
 4: /cgn2\_6/pktodata/2/pubpna/us05\_pubcomb.seq:  
 5: /cgn2\_6/pktodata/2/pubpna/us05\_new\_pub.seq:  
 6: /cgn2\_6/pktodata/2/pubpna/pctns\_pubcomb.seq:  
 7: /cgn2\_6/pktodata/2/pubpna/us04\_new\_pub.seq:  
 8: /cgn2\_6/pktodata/2/pubpna/us03\_pubcomb.seq:  
 9: /cgn2\_6/pktodata/2/pubpna/us02\_new\_pub.seq:  
 10: /cgn2\_6/pktodata/2/pubpna/us09\_pubcomb.seq:  
 11: /cgn2\_6/pktodata/2/pubpna/us10\_new\_pub.seq:  
 12: /cgn2\_6/pktodata/2/pubpna/us10\_pubcomb.seq:  
 13: /cgn2\_6/pktodata/2/pubpna/us01\_new\_pub.seq:  
 14: /cgn2\_6/pktodata/2/pubpna/us05\_pubcomb.seq:  
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Pred NO is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Match Length	DB ID	Description
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2	975.8	71.1	2143	10	US-09-410-194-16
3	858.2	62.5	1190	10	US-09-410-194-14
4	373.8	27.2	2452	10	US-09-410-194-18
c 5	354.2	25.8	490	10	US-09-833-381-36
c 6	337.8	24.6	2770	9	US-09-005-921-1
c 7	276	20.1	437	10	US-09-864-761-3120
c 8	177	12.9	177	10	US-09-864-761-19899
c 9	90	6.6	277	10	US-09-960-352-12673
c 10	88	6.4	200	9	US-10-005-921-4
c 11	80.2	5.8	416	10	US-09-960-352-4584
c 12	79.4	5.8	312	10	US-09-960-352-8414
c 13	79.4	5.8	375	10	US-09-960-352-5014
c 14	79.4	5.8	424	10	US-09-960-352-11218
c 15	79.2	5.8	272	10	US-09-960-352-6986
c 16	78	5.7	393	10	US-09-960-352-4582
c 17	77.4	5.6	408	10	US-09-960-352-6263
c 18	77.2	5.6	373	10	US-09-960-352-8836
c 19	77.2	5.6	3899	10	US-09-745-763-107

**ALIGNMENTS**

RESULT 1  
US-09-861-270-1  
Sequence 1, Application US-09861270  
; Patent No. US20020052474A1  
; GENERAL INFORMATION:  
; APPLICANT: Sui, Hong-Bing  
; GOEDDEL, David V.  
; TITLE OF INVENTION: Regulators of Apoptosis  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Science & Technology Law Group  
; STREET: 75 Denise Drive  
; CITY: Hillsborough  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94010

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version # 1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US-09-861-270-1  
FILING DATE: 18-May-2001  
PRIORITY APPLICATION NUMBER: 08/795,088  
ATTORNEY/AGENT INFORMATION:  
NAME: Oshani, Richard A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342.  
INFORMATION FOR SEQ ID NO: 1;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2045 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

;	SEQUENCE DESCRIPTION: SEQ ID NO: 1:							
us-09-861-270-1								
Query Match	74.7%;	Score 1025.2;	DB 10;	Length 2045;				
Best Local Similarity	99.6%;	Pred. No. 2.9e-202;						
Matches 1038;	Conservative 0;	Mismatches 3;	Indels 1;	Gaps 1;				
					RESULT 2			
	48 GCGAGCTTGCAGCCCTCACCGACGAGTCCTAACCTAAAGGGACTCCGGAGCTAGGGGTG 107		Db 1037 AAGGAGCAGGGACAAGTTACAGGAATGTTCTCAAGCAATCCAAGGAGCAATCTCAAGG 1096					
	Db 78 GAGACCTTGAGCCCTCACCGACGAGTCCTAACCTAAAGGGACTCCGGAGCTAGGGGT 137		Qy 1068 ATCCCTCAATACTACTTCAGGAT 1089					
	Qy 108 GGACTCGGGCTCACACAGTAGTCAGTGAGTCGGGATATTGACATTGTCAGTACACTGAC 167		Db 1069 ATCCCTCAATACTTCAGGCT 1118					
	Db 138 GGACTCGGGCTCACACAGTAGTCAGTGAGTCGGGATATTGACATTGTCAGTACAGTGAC 197							
	Qy 168 AACAGGACCAACGGAGGGAGGTAGGAGAAGCAGGCCGAACAGCAGATGCCAGAAC 227							
	Db 198 AACAGGACCAACGGAGGGAGGTAGGAGAAGCAGGCCGAACAGCAGATGCCAGAAC 257							
	Qy 228 CAAAGTCCGGCTTCCAGGCTTTCGGTTCTGGCTTCCACATTTGGCTGGCTTCGGGT 287							
	Db 258 CTAAGGGAGCGGAAGGCTGAGGTCTGGGTTCTGGCTTCACATTTGGCTGGCTTCGGGT 317							
	Qy 288 CTAGGGAGCGGAAGGCTGAGGTCTGGGTTCTGGCTTCACATTTGGCTGGCTTCGGGT 347							
	Db 318 Db 318 CTAGGGAGCGGAAGGCTGAGGTCTGGGTTCTGGCTTCACATTTGGCTGGCTTCGGGT 377							
	Qy 348 CCCCCACTGAAAGGATTCTGAAAGAAGTCAGCCCTCAGAAATAAGTGAATC 407							
	Db 378 CCCCCACTGAAAGGATTCTGAAAGAAGTCAGCCCTCAGAAATAAGTGAATC 437							
	Qy 408 CTGCGGGCTTCCGTTCTGGACTGGCCGGAGCTGACTGGAAACCCCTTGAGTTCCCT 467							
	Db 438 CTGCGGGCTTCCGTTCTGGACTGGCCGGGGCTGACTGGAAACCCCTTGAGTTCCCT 496							
	Qy 468 AGTCTAAGACTAGGATGTTCTGCTGAAGTCATCCATCAGGTGAAGAACCTGTATA 527							
	Db 497 AGTCTAAGACTAGGATGTTCTGCTGAAGTCATCCATCAGGTGAAGAACCTGTATA 556							
	Qy 528 ATGAGAAGGAGATGCTGCTCTTGTGCGGGGATGTTCTATGATGTTGCTTACCTA 587							
	Db 557 ATGAGAAGGAGATGCTGCTCTTGTGCGGGGATGTTCTGTTGCTTACCTA 616							
	Qy 588 ATGTCAGGGACCTCTGGATATTAGCGAAAGAGCTGTCGCGGGACTCTG 647							
	Db 617 ATGTCAGGGACCTCTGGATATTAGCGAAAGAGCTGTCGCGGGACTCTG 676							
	Qy 648 CTGAACCTGCTACAGAGTAGGGGATTGACCTGCTCAAACGATCTGAGATGAGA 707							
	Db 677 CTGAACCTGCTACAGAGTAGGGGATTGACCTGCTCAAACGATCTGAGATGAGA 736							
	Qy 708 GAAAAGCTTGTGAGAACCCACTGTCAGGAACTCTGTCAGGACTATAGAGTC 767							
	Db 737 GAAAAGCTTGTGAGAACCCACTGTCAGGAACTCTGTCAGGACTATAGAGTC 796							
	Qy 768 TGATGGCAGAGATGGTAGGATTGGATTAATCTGATCTGTCAGGAACTCTGTCAGGACTATAGAGTC 827							
	Db 797 TGATGGCAGAGATGGTAGGATTGGATTAATCTGATCTGTCAGGAACTCTGTCAGGACTATAGAGTC 856							
	Qy 828 TGAAGGATTAATGGCCAGGCAAGATAGCAAGGAGAGTTCTGGACCTTGTGG 887							
	Db 857 TGAAGGATTAATGGCCAGGCAAGATAGCAAGGAGAGTTCTGGACCTTGTGG 916							
	Qy 888 TTGAGTTGAGAACTAAATTGGTGCCTCAGGAACTCTGGATTATAGAAATAATGCC 947							
	Db 917 TTGAGTTGAGAACTAAATTGGTGCCTCAGGAACTCTGGATTATAGAAATAATGCC 976							
	Qy 948 TAAAGAACATCCACAGAAATGACCTGAGAACAAAATCAGAAACTPACAAGCAGCTGTC 1007							
	Db 977 TAAAGAACATCCACAGAAATGACCTGAGAACAAAATCAGAAACTPACAAGCAGCTGTC 1036							
	Qy 1008 AAGGAGGAGGACAACTTACAGGAATGTTCTCCAAAGGAAATCAGAAAGTCAGA 1067							
	Db 1037 AAGGAGCAGGGACAAGTTACAGGAATGTTCTCCAAAGGAGCAATCTCAAGG 1096							
	Qy 1068 ATCCCTCAATACTTCAGGAT 1089							
	Db 1069 ATCCCTCAATACTTCAGGCT 1118							
	Qy 1070 ATCCCTCAATACTTCAGGCT 1118							
	Db 1071 ATCCCTCAATACTTCAGGCT 1118							
	Qy 1072 ATCCCTCAATACTTCAGGCT 1118							
	Db 1073 ATCCCTCAATACTTCAGGCT 1118							
	Qy 1074 ATCCCTCAATACTTCAGGCT 1118							
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	Qy 1092 ATCCCTCAATACTTCAGGCT 1118							
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	Qy 1100 ATCCCTCAATACTTCAGGCT 1118							
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	Qy 1108 ATCCCTCAATACTTCAGGCT 1118							
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	Qy 1110 ATCCCTCAATACTTCAGGCT 1118							
	Db 1111 ATCCCTCAATACTTCAGGCT 1118							
	Qy 1112 ATCCCTCAATACTTCAGGCT 1118							
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	Qy 1114 ATCCCTCAATACTTCAGGCT 1118							
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	Qy 1128 ATCCCTCAATACTTCAGGCT 1118							
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	Qy 1188 ATCCCTCAATACTTCAGGCT 1118							
	Db 1189 ATCCCTCAATACTTCAGGCT 1118							
	Qy 1190 ATCCCTCAATACTTCAGGCT 1118							
	Db 1191 ATCCCTCAATACTTCAGGCT 1118							
	Qy 1192 ATCCCTCAATACTTCAGGCT 1118							
	Db 1193 ATCCCTCAATACTTCAGGCT 1118							

Db	360	AGCTTCCCTAGTCTAAGAGTAGGATGTCAGGTCAATCAGGTGAGAACAC 419	;	ORGANISM: Homo sapiens
Qy	519	TTGATACAGATGAAAGGATGCTGGCTCTTTGTGCCGGATGTGCTATAAGATGTGG 578	;	FEATURE: CDS
Db	420	TTGATACAGATGAAAGGATGCTGGCTCTTTGTGCCGGATGTGCTATAAGATGTGG 479	;	NAME/KEY: (394)...(1056)
Qy	579	TTCCACCTATGTCAGGACCTCTGGTATTTACGGAAAGGTAAGCGTCTGTCG 638	;	LOCATION: US-09-410-194-14
Db	480	TTCCACCTATGTCAGGACCTCTGGTATTTACGGAAAGGTAAGCGTCTGTCG 539	;	Query Match Score: 62.5%; Best Local Similarity: 99.5%; Pred. No. 6.7e-168; Mismatches: 3; Indels: 1; Gaps: 1;
Qy	639	GGGACTTGGCTGAACCTCTACAGAGTAGGGATTGACCTGCTCAAACCTATCTGA 698	;	Matches: 871; Conservative: 0; Gaps: 1;
Db	540	GGGACTTGGCTGAACCTCTACAGAGTAGGGATTGACCTGCTCAAACCTATCTGA 599	;	Query Match Score: 62.5%; Best Local Similarity: 99.5%; Pred. No. 6.7e-168; Mismatches: 3; Indels: 1; Gaps: 1;
Qy	699	AGATGGACAAAGCTGGGACCCACTCTGGTCAAGAACCTCACCTGTCAGGACT 758	;	Matches: 871; Conservative: 0; Gaps: 1;
Db	600	AGATGGACAAAGCTGGGACCCACTCTGGTCAAGAACCTCACCTGTCAGGACT 659	;	Query Match Score: 62.5%; Best Local Similarity: 99.5%; Pred. No. 6.7e-168; Mismatches: 3; Indels: 1; Gaps: 1;
Qy	759	ATAGAGTCTGTATGGCAGAGATGGTGGATAAATCTGATGTCCTCATTA 818	;	Matches: 871; Conservative: 0; Gaps: 1;
Db	660	ATAGAGTCTGTATGGCAGAGATGGTGGATAAATCTGATGTCCTCATTA 719	;	Query Match Score: 62.5%; Best Local Similarity: 99.5%; Pred. No. 6.7e-168; Mismatches: 3; Indels: 1; Gaps: 1;
Qy	819	TTCCTCTATGAAAGGATTACATGGCCSAGGGAAAGATAAGCAGGGAGGTTCTTG 878	;	Matches: 871; Conservative: 0; Gaps: 1;
Db	720	TTCCTCTATGAAAGGATTACATGGCCSAGGGAAAGATAAGCAGGGAGGTTCTTG 779	;	Query Match Score: 62.5%; Best Local Similarity: 99.5%; Pred. No. 6.7e-168; Mismatches: 3; Indels: 1; Gaps: 1;
Qy	879	ACCTGTGTGGTGAAGTGGAAACTAAATTGGTTGCCAGATCAACTGGATTATAG 938	;	Matches: 871; Conservative: 0; Gaps: 1;
Db	780	ACCTGTGTGGTGAAGTGGAAACTAAATTGTGGTTGCCAGATCAACTGGATTATAG 839	;	Query Match Score: 62.5%; Best Local Similarity: 99.5%; Pred. No. 6.7e-168; Mismatches: 3; Indels: 1; Gaps: 1;
Qy	939	AAAATGGCTAAAGAACATCCAGAAATGACCTGAACAAATACTGGCTAACAGC 998	;	Matches: 871; Conservative: 0; Gaps: 1;
Db	840	AAAATGGCTAAAGAACATCCAGAAATGACCTGAACAAATACTGGCTAACAGC 899	;	Query Match Score: 62.5%; Best Local Similarity: 99.5%; Pred. No. 6.7e-168; Mismatches: 3; Indels: 1; Gaps: 1;
Qy	999	AGTCGTGTCAGGAGCAGGACAAAGTTAGGAAATGTTCTCCAGCACAATCCAALAGA 1058	;	Matches: 871; Conservative: 0; Gaps: 1;
Db	900	AGTCGTGTCAGGAGCAGGACAAAGTTAGGAAATGTTCTCCAGCACAATCCAALAGA 959	;	Query Match Score: 62.5%; Best Local Similarity: 99.5%; Pred. No. 6.7e-168; Mismatches: 3; Indels: 1; Gaps: 1;
Qy	1059	GTCICAAGGATCCCTCAATAACTTCAGGT 1089	;	Matches: 871; Conservative: 0; Gaps: 1;
Db	960	GTCICAAGGATCCCTCAATAACTTCAGGT 990	;	Query Match Score: 62.5%; Best Local Similarity: 99.5%; Pred. No. 6.7e-168; Mismatches: 3; Indels: 1; Gaps: 1;
<b>RESULT 3</b>				
US-09-410-194-14				
Sequence 14 Application US/09410194				
Patent No. US20030095030A1				
GENERAL INFORMATION:				
APPLICANT: Tschopp, Jurg				
APPLICANT: Thomé, Margot				
APPLICANT: Burris, Kimberly				
APPLICANT: Irmier, Marten				
APPLICANT: Hahne, Michael				
APPLICANT: Schreiter, Michael				
APPLICANT: Schneider, Pascal				
APPLICANT: Bodmer, Jean-Luc				
APPLICANT: Steiner, Veronique				
APPLICANT: Rimoldi, Donata				
APPLICANT: Hofmann, Kay				
APPLICANT: French, E. Lars				
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS				
FILE REFERENCE: 11141-002001				
CURRENT FILING DATE: 1998-09-10				
PRIORITY APPLICATION NUMBER: PCT/EP98/01857				
PRIOR FILING DATE: 1998-03-31				
PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2				
PRIOR FILING DATE: 1997-04-01				
NUMBER OF SEQ ID NOS: 27				
SOFTWARE: FastSPS for Windows version 4.0				
SEQ ID NO: 14				
LENGTH: 1190				
TYPE: DNA				
RESULT 4				
US-09-410-194-18				
US-09-410-194-14				
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US-09-410-194-14				
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US-09-410-194-14				
US/0				

Sequence 18, Application US/09410194  
 Patent No. US020095030A1  
 GENERAL INFORMATION:  
 APPLICANT: 'tschopp, Jurg  
 APPLICANT: Thome, Marcot  
 APPLICANT: Burns, Kimberly  
 APPLICANT: Irmler, Marion  
 APPLICANT: Hahne, Michael  
 APPLICANT: Schröter, Michael  
 APPLICANT: Schneider, Pascal  
 APPLICANT: Bodmer, Jean-Luc  
 APPLICANT: Steiner, Veronique  
 APPLICANT: Rimoldi, Donata  
 APPLICANT: Hofmann, Kay  
 APPLICANT: French, E.  
 TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS  
 FILE REFERENCE: 1114-002001  
 CURRENT APPLICATION NUMBER: US/09/410.194  
 CURRENT FILING DATE: 1999-09-30  
 PRIOR APPLICATION NUMBER: PCT/EP98/01857  
 PRIOR FILING DATE: 1998-03-31  
 PRIOR APPLICATION NUMBER: DE 1998 13 393.2  
 PRIOR FILING DATE: 1997-04-01  
 NUMBER OF SEQ ID NOS: 27  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 18  
 LENGTH: 2452  
 TYPE: DNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (172) . . . (1614)  
 US-09-410-194-18

Query Match Score 373.8; DB 10; Length 2452;  
 Best Local Similarity 68.8%; Pred. No. 9.8e-68; Gaps 1;  
 Matches 532; Conservative 0; Mismatches 232; Indels 9; Gaps 1;

Qy 313 AGCGGAGGAGACTGGGCCGACAGGACAACTCCCCACTGGAAAAGGATTCTGAAG 372  
 Db 9 AGCCCTCAAGGGCRACTTAGGCCGACAGAGTGTCTATTCGAGAACTCTGAGAG 68

Qy 373 AAATGAGTCAGCCCTCGAAATGAGTTGACTGCCCTGG-----CTTCTGT 423  
 Db 69 AAATGAGAGTCTCCAGCATGCCCTTGCTGTTCTCGTGTGCTTA 128

Qy 424 TGACTGCCGCGACTCGCAAGACCCCTGGTGAAGTAGCTTAAGAGTAGGAT 483  
 Db 129 TGGATGGAGACTGGAGGAGCTGGTGCCTGTTGACATGCCAGGCCCTGT 188

Qy 484 GTCTGCTGAAGTCATCCATCAGGTGAAGAGCAGTGTATAAGATGAGGAGATGCT 543  
 Db 189 GTCTGCGAGETCATTCACAGGTGGACTGAGTGTGAGAACCTGAGGAGATGAT 248

Qy 544 GGATATTACGGGAAGAGGTAACTGGTGGGACTGTGGTGAAGTCCTACAG 663  
 Db 309 GGATGCTTAAGTGGAGAGCCTGCTACCTTGACTGGCAATGTGCTACAG 368

Qy 664 AGTGGCGATTGACTGCTCAAAGTATCTGAGTGAAGAGCTGTGGAGAC 723  
 Db 369 AGTGGCGGTTGACCTTCAGAGGATCTGAGACAGACAAGAACCGTGGAGGA 428

Qy 724 CCACCTGCTCAAGAACCTCACCTTGACTGGACATAGTGTGGAGATTACATGG 843  
 Db 429 CCACCTGCGAACCTCACCTGCTTCAGAGGATCTGAGACAGACAAGAAC 488

Qy 784 TGAGGATTGGATAAATCTGATGTCNCTCATTAAATTCTCTCATGAAGGATTACATGG 843  
 Db 489 TGAGGCTTAACTGAAACCTGATGGCTTCTCTTCAAGGGATTACAGCAG 548

Qy 844 CGAGGCAAGATAAGCAAGGAGAAAGAGTTGACTGGCTTGAGCTTGAGAAACT 903  
 Db 549 CAGGGCAAGATAGCCAGAGTGTCTGGATCTGGATCTGGATGAACTGGAAACT 608

Qy 904 AATPTGGTGGCCCGAGATTAACCTGAGTATTAGAAAATGCTTAAGGACATCCAG 963  
 Db 609 GAAVCTAATGCTTCAGACCAATTGAATTGCTTAAGGACATCCAG 668

Qy 964 AATAGACCTGAAAGACAAAAATCCAGAGTACAAGGAGTCCTCAAGGAGCAAG 1023  
 Db 669 ATAGACCTGAAAGACACAAGGAGTACCCAGTCAGCCAGAGAAGTCAA 728

Qy 1024 TTACAGGAATGTTCTCCAARGCAATCCAAAAGGACTCTAAAGGATCCTCAA 1076  
 Db 729 TATGATACUTCTCCAGGTCGCTCCAAATTGACTAACAGTAACTCAA 781

RESULT 5  
 US-09-833-381-436/C  
 Sequence 436, Application US/09833381  
 ; Patent No. US2002132050A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robison, Keith E.  
 ; ATTORNEY: Robison, Keith E.  
 ; TITLE OF INVENTION: No. US2002132050A1 Nucleic Acid and Protein Homologs  
 ; FILE REFERENCE: 5800-119  
 ; CURRENT APPLICATION NUMBER: US/09/833,381  
 ; CURRENT FILING DATE: 2001-04-11  
 ; PRIORITY APPLICATION NUMBER: 09/516,448  
 ; PRIORITY FILING DATE: 2000-02-29  
 ; NUMBER OF SEQ ID NOS: 2050  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 436  
 ; LENGTH: 490  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(490)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-09-833-381-436

Query Match Score 354.2; DB 10; Length 490;  
 Best Local Similarity 82.4%; Pred. No. 5.1e-34;  
 Matches 404; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 653 CTGCCTACAGACTGAGGGATTGACCTGTCTAACAGTATCTTGRAGATGGACAGAAA 712  
 Db 490 CTGTCATAGAGTGGGCCATTGATGGCTCATGCTCTCGACATCGACARACA 431

Qy 713 GCTGGAGACCCACCTGCTCAGGAACCCCTACACCTGTTGGACTATAGTGTGATG 772  
 Db 430 GCTGTCAGATCCACNTGCTAGCCATCTCACATGCTGACTATACAGTGTGATG 371

Qy 773 GCAGAGATGGTGGAGATTGGATAATCTGATGPGTCCCATTAATTTCCTCATGAG 832  
 Db 370 GTACAGATCTGGTGGCCATTCGATCAATNCATGTCCTCATTCATTCTTATCAAG 311

Qy 833 GATPACATGGCCGAGGCCAGATAAGCAAGGAGAAAGTTCTTGGACCTTGTGGTGA 892  
 Db 310 CATCCAATGCCCCTGGTAGATAACCCAGGAGAGTTTTGGACTTGTGGTGA 251

Qy 893 TTGGAAARCTAAATTGGTGGCCCATTAATTTCCTCATGAGAGTTTTGGACTTGTGGTGA 952  
 Db 250 TTGGAGAARNTACATCGGTCGCTCAGATCTAGTCATTCAGCAATATGCTTAAG 191

Qy 953 AACATCCACAGATAAGCTGCAAAATCCAGAAAGTACAAAGCAGTCTGTTCAAGGA 1012  
 Db 190 AACATCCACAGATAAGCTGCAAAATCCAGAAAGTACAAAGCAGTCTGTTCAAGCA 131

Qy 1013 GCGGGACAGTTACAGGATGTCAGTGTCTCATTAAATTCTCTCATGAAGGATTACATGG 1072  
 Db 130 GCAGGACAGTCAAGGATGTCAGTGTCTCATTAAATTCTCTCATGAAGGATTACATGG 71

Qy 1073 TCAAATAACTTCAGGATGATAAACCCCTPATGCCCATGTCCTGATCTGAAATTCTTGGAA 1132  
 Db 70 TTAAATAATTTCAGGATGATCACACCCCTATGCCCATGTGCTGATTGAAATTTTGGC 11  
 Qy 1133 AATGGTCCA 1142  
 Db 10 CATGGTCCA 1

RESULT 6  
 US-10-005-921-1  
 ; Sequence 1, Application US/10005921  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Levitan, Michael W.  
 ; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CASH GENE  
 ; TITLE OF INVENTION: DISRUPTIONS  
 ; FILE REFERENCE: R-714  
 ; CURRENT APPLICATION NUMBER: US/10/005,921  
 ; CURRENT FILING DATE: 2001-12-04  
 ; PRIOR APPLICATION NUMBER: US 60/254,902  
 ; PRIOR FILING DATE: 2000-12-11  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 2770  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; US-10-005-921-1

Query Match Best Local Similarity 24.6% score 337.8; DB 9; Length 2770;  
 Matches 451; Conservative 0; Mismatches 157; Indels 9; Gaps 1;

Qy 469 GTCTAAGTAGATGGATGCTGAAGTCATCATCAGTGAAGAACCTGTGATACAGA 528  
 Db 77 GGCCCAGGCCNGTGCTGCCAGGGTCATTCACCAGTGGAGACTGTGATGAA 136  
 Qy 529 TGAAAGGGAGATGGCTGCTGGGGATGCTGGATGCTAGATGAGTGGTCCACCTAA 588  
 Db 137 CGAGAAGGGAGATGATGCTCTCTGTGAGATGTGACTGTGAAACCTGGTGCACCTAA 196  
 Qy 589 TGTCAAGGGACCTCTGGATATTACCGGAAAGAGTAAGGTTGCTGCTGGGACTTGGC 648  
 Db 197 CGTCAGGGACCTCTGGATAGCTTAAGTGAAGCTTGTGACCTTGTGACCTTGGC 256  
 Qy 649 TGAAGCTGCTCTACAGATGAGGGATTGACCTGCTCAAACGTATCTGAAAGTGGACAG 708  
 Db 257 TGAATTCGCTCTACAGATGAGGGATTGACCTCTCAAGAGATCTGAAAGCACAA 316  
 \*Qy 709 AAAGCTGTGAGAACCCACTGTGCTGAAACCTGACTGTGACTATAGAGTGGCT 768  
 Db 317 AGCAACCCGGAGGACCACTCTGGCAGAAACCTCTACCTGGTCTCATTTAGGGTCC 376  
 Qy 769 GATGGCAAGATGGTGGAGATGATAATTCTGTTGCTCAATTATTTCC----- 824  
 Db 377 GCTGATGGGATGTTGAGGTTAGATCAGACGAGTACCTCTCTTAGTTTCCTTAC 436  
 Qy 825 -----TCATGAAGGATTACATGGCCGAGGCAAGATAACGAGGAAAGAGTTCTTGGA 879  
 Db 437 AAGGATTACAAAGGATTACACGGCAGGCAAGATGCAAGGAAAGGTTCTTGGA 496  
 Qy 880 CCTTGTTGGTGTGAGTTGGGAAACTAAATTGGTGCCTCAGATRACTGTTTATAGA 939  
 Db 497 TCCTGGTGTGATGAAATTGGGAAACTGAATCTGAACTTGTGAAATTGGTCTGAGA 556  
 Qy 940 AAAATGCCAAAGAACATCACAGAAATGACCTGAAAGTACAGAA 999  
 Db 557 AAAATGCCAAAGAACATCACAGAAATGACCTGAAAGTACACCA 616  
 Qy 1000 GTCCTGGTCAAGGGACAGTTACGGAAATGTTCTCCAGGCAATCCAAAAGAG 1059

Db 617 GTCAGGCCAAGGCAAGATCAATATGAAATCTCCAGGCTCCAAATTTGAG 676  
 Qy 1060 TCTCAAGGATCTCTCAAATGAACTCTCCAGGCTCCAAATTTGAG 676  
 Db 677 TATCAAGTATACTCAA 693

RESULT 7  
 US-09-864-761-3120/C  
 ; Sequence 3120, Application US/09854761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
 ; FILE REFERENCE: Aeomica-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: US 60/734,687  
 ; PRIOR FILING DATE: 2000-09-21  
 ; PRIOR APPLICATION NUMBER: US 09/608,408  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 09/774,203  
 ; PRIOR FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 49117  
 ; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
 ; SEQ ID NO 3120  
 ; LENGTH: 437  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5  
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8  
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2  
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1  
 ; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.9  
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3  
 ; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN BT74, SIGNAL = 2.6  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2  
US-09-864-761-3120

Query Match Score 276; DB 10; Length 437;  
Best Local Similarity 100.0%; Pred. No. 6.0e-48;  
Matches 276; conservative 0; Mismatches 0; Gaps 0;  
Indels 0;

Qy 487 TGCCTGAAGTCATCCATTACGGTGGAAACGACTGATAAGTAGAGAAGGAGATGCTGT 546  
Db 437 TGCTGAAGTCATCCATTACGGTGGAAACGACTGATAAGTAGAGAAGGAGATGCTGT 378

Qy 547 CTTTTGTGCCGGATGTTGCTATAGATGGTTCACCTTAATCAGGACCCWTCGGA 606  
Db 377 CTTTTGTGCCGGATGTTGCTATAGATGGTTCACCTTAATCAGGACCCWTCGGA 318

Qy 607 TATTTCACGGAAAGAGGTAAAGCTGCTGTCTGGGACATGGCTCACTCTCATAGAGT 666  
Db 317 TATTTCACGGAAAGAGGTAAAGCTGCTGTCTGGGACATGGCTCACTCTCATAGAGT 258

Qy 667 GAGGGGATTTGACCTGCTAAACGTATCTGATGTCAGATGCCAGAAAAGCTGTGGACCCA 726  
Db 257 GAGGGGATTTGACCTGCTAAACGTATCTGATGTCAGATGCCAGAAAAGCTGTGGACCCA 198

Qy 727 CCTGCTCAGGAACCCTCACCTGGTTGGACTATAGT 762  
Db 197 CCTGCTCAGGAACCCTCACCTGGTTGGACTATAGT 162

**RESULT 8**  
US-09-864-761-19899/c  
Sequence 19899, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Weisheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aeonlica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1  
SEQ ID NO 19899  
FEATURE:  
ORGANISM: Homo sapiens  
LENGTH: 177

OTHER INFORMATION: MAP TO AC007272 2  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9  
OTHER INFORMATION: EXPRESSED IN HEK293, SIGNAL = 3.3  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.5  
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.6  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2  
OTHER INFORMATION: SWISSPROT HIT: Q51391, EVALUATE 4.90e+00  
OTHER INFORMATION: EST HUMAN HIT: AV691851.1, EVALUATE 3.00e-95  
US-09-864-761-19899

Query Match Score 177;  
Best Local Similarity 100.0%; Pred. No. 1.2e-27;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 482 ATGTCGCTGAACTCCATCGGTGAAAGAACCTTGATGAGAAGGAGATG 541  
Db 177 ATGTCGCTGAACTCCATCGGTGAAAGAACCTTGATGAGAAGGAGATG 118

Qy 542 CTGGATATTTCACGGAAAGAGGTAACTGTCGGGGACTPTGGCTGAACCTT 601  
Db 117 CTGGATATTTCACGGAAAGAGGTAACTGTCGGGGACTPTGGCTGAACCTT 58

Qy 602 CTGGATATTTCACGGAAAGAGGTAACTGTCGGGGACTPTGGCTGAACCTT 658  
Db 57 CTGGATATTTCACGGAAAGAGGTAACTGTCGGGGACTPTGGCTGAACCTT 1

**RESULT 9**  
US-09-960-352-12673/c  
Sequence 12673, Application US/09960352  
Patent No. US20020137139A1  
GENERAL INFORMATION:  
APPLICANT: Warren, Wesley C.  
APPLICANT: Tao, Ningbing  
APPLICANT: Byatt, John C.  
APPLICANT: Mathialagan, Nagappan  
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION A  
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION  
FILE REFERENCE: 1651.006/37-21(1098)C  
CURRENT APPLICATION NUMBER: US/09/960,352  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 15112  
SEQ ID NO 12673  
LENGTH: 277

Query Match Score 90; DB 10; Length 277;  
Best Local Similarity 64.3%; Pred. No. 1.4e-09;  
Matches 135; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

US-09-960-352-12673

OTHER INFORMATION: Clone ID: 20-LIB3057-016-01-K1-E11 US-09-960-352-4584									
Query	Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Ind.
Qy 1121 AAAATTCTCGAAATTGTCATGGTAAACATGGAACTGCCTCTAG	Db 274 AATTTCTCTTAAATTAATTTTTTTTTTTTTTTTTTTTTTTTT	5.8%	DB 10;	Len 0;	Matches 145; Conservative 0;	Pred. No. 1.8e-07;	0;	Mismatches 108;	Ind. 1
Qy 1181 ARTGATTAAATCCTGGTCAATTCTAATAGTGTATAAATGTTAGGCC	Db 214 TTAATTTTATATTTAAATTCTTTAAACCTTTTTTTTTTTTTTT	5.8%	DB 10;	Len 0;	Matches 145; Conservative 0;	Pred. No. 1.8e-07;	0;	Mismatches 108;	Ind. 1
Qy 1241 TGTATGTTAGATGCTTCCAATCTTGTACTACTAAATGCTATA	Db 154 TTATTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	5.8%	DB 10;	Len 0;	Matches 145; Conservative 0;	Pred. No. 1.8e-07;	0;	Mismatches 108;	Ind. 1
Qy 1301 CTTGFACTCTTAAAAAAAAATTTTTTTTTTTTTTTTTTTTT	Db 94 TTTTTTTTTTTTAAADAAATAAAAAAATPACCAACCAAAAT	5.8%	DB 10;	Len 0;	Matches 145; Conservative 0;	Pred. No. 1.8e-07;	0;	Mismatches 108;	Ind. 1
Qy 1361 AAAAAAAAAAAA 1373	Db 34 AAAAAAAAAAAA 22	5.8%	DB 10;	Len 0;	Matches 145; Conservative 0;	Pred. No. 1.8e-07;	0;	Mismatches 108;	Ind. 1
<b>RESULT 12</b>									
US-09-960-352-8414/C	Sequence 8414 ; Application US/09960352	5.8%	DB 10;	Len 0;	Matches 145; Conservative 0;	Pred. No. 2.3e-07;	0;	Mismatches 71;	Ind. 1
Patent No. US20020137139A1	GENERAL INFORMATION:								
APPLICANT: Warren, Wesley C.	APPLICANT: Tao, Ningbing								
APPLICANT: Bhatt, John C.	APPLICANT: Mathialagan, Nagappan								
APPLICANT: Mathialagan, Nagappan	TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES AS								
FILE REFERENCE: 16511.106/37-21(10268)C	TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION								
CURRENT APPLICATION NUMBER: US/09/960,352	FILE REFERENCE: 16511.106/37-21(10268)C								
NUMBER OF SEQ ID NOS: 15112	CURRENT FILING DATE: 2001-09-24								
SEQ ID NO: 8414	SEQUENCE FILING DATE: 2001-09-24								
LENGTH: 312	NUMBER OF SEQ ID NOS: 15112								
TYPE: DNA	SEQUENCE ID NO: 8414								
ORGANISM: Bos taurus	SEQUENCE LENGTH: 312								
OTHER INFORMATION: Clone ID: 36-LIB3058-048-01-K1-A8	OTHER INFORMATION: Clone ID: 36-LIB3057-016-01-K1-E11								
US-09-960-352-8414	US-09-960-352-8414	5.8%	DB 10;	Len 0;	Matches 145; Conservative 0;	Pred. No. 2.3e-07;	0;	Mismatches 71;	Ind. 1
<b>RESULT 13</b>									
Query	Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Ind.
Qy 1176 TTTCGAATTGATTAATCTGGTCATTCTAAATGTTATAAATGTT	Db 223 TTTCGCGATTGTTGATTGTTGATTGTTGATTGTTGATTGTTGTT	5.8%	DB 10;	Len 0;	Matches 122; Conservative 122;	Pred. No. 2.3e-07;	0;	Mismatches 71;	Ind. 1
Qy 1236 GTTGCTGTATGTTAGATGCTTCCAACTTTGTTACTAATATAA	Db 163 TTTCGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT	5.8%	DB 10;	Len 0;	Matches 122; Conservative 122;	Pred. No. 2.3e-07;	0;	Mismatches 71;	Ind. 1
Qy 1296 ATATCCTGTGACTCTTAAATTTTTTTTTTTTTTTTTTTTT	Db 103 ATAAAAAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAA	5.8%	DB 10;	Len 0;	Matches 122; Conservative 122;	Pred. No. 2.3e-07;	0;	Mismatches 71;	Ind. 1
Qy 1356 AAAAAAAAAAAA 1368	Db 43 AAAAAAAAAAAA 31	5.8%	DB 10;	Len 0;	Matches 122; Conservative 122;	Pred. No. 2.3e-07;	0;	Mismatches 71;	Ind. 1

```

; Sequence 15014, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Bryant, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21 (10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 15014
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 64-LIB3058-048-Q1-K1-148
US-09-960-352-15014

Query Match      5.8%; Score 79.4; DB 10; Length 375;
Best Local Similarity 64.3%; Pred. No. 2.5e-07;
Matches 119; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy  1189 AATCGTTTCATTTCTAAATGTTTAATGTTTAATGTTAGCCCTTCTGTGCTGATGTT 1248
Db  274 ATTTTTAAATTTTTTTTTTTTTTCCATCCCTTTTTAAAAAAATAA 215

Qy  1249 TAGATGGTTCCAAATCTTTGTTACTAAATAATGCTATAAAATAATCCTGTACT 1308
Db  214 TATATTTTTTTTTTTTTTTAAATAAAAATAATAAAAATAATAAA 155

Qy  1309 TCCTAAAAAAAGAAAAAAAGAAAAAAAGAAAAAAAGAAAAAAAGAAAAAA 1368
Db  154 TAAAGAAATATATAAAGAAAAAAAGAAAAAAAGAAAAAAAGAAAAAA 95

Qy  1369 AAAAA 1373
Db  94 AAAAA 90

RESULT 14
US-09-960-352-11218/C
; Sequence 11218, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Bryant, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21 (10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11218
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 48-LIB3058-026-Q1-K1-D12
US-09-960-352-11218

Query Match      5.8%; Score 79.4; DB 10; Length 424;
Best Local Similarity 57.4%; Pred. No. 2.6e-07;
Matches 143; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

Qy  1125 TTCTGGAAATGTTCCATGTCATACATGGAACTGCCCTACTTAATCTGAATG 1184
Db  270 TTCTTAAATATCTCTTTTAAATTCCCTATAATTCTTAT 211

Qy  1185 ATTAATCTGGTTCAATTCTAAATGTTAGCCCTTCCTGTTGCTGTT 1244

```



ATTORNEY/AGENT INFORMATION:  
 NAME: Osman, Richard A  
 REGISTRATION NUMBER: 36,627  
 REFERENCE/DOCKET NUMBER: T97-001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 343-4341  
 TELEFAX: (650) 343-4342  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2045 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-795-088A-1

Query Match Score 1025.2; DB 4; Length 2045;  
 Best Local Similarity 99.6%; Pred. No. 8.9e-227;  
 Matches 1038; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 48 GCGAGCTTGCAAGCTCACCGAGGAGTCACACTAAANGGACTCCCGAGGTAGGGTGG 107  
 Db 78 GAGAGCTGCAAGCTCACCGAGGAGTCACACTAAAGGACTCCCGAGGTAGGGTGG 137

Qy 108 GGACTCGGCCCTACACAGTGTGCAGCTATTGGACTTTGTCAGTGACAGCTGAGAC 167  
 Db 138 GGACTCGGCCCTACACAGTGTGCAGCTATTGGACTTTGTCAGTGACAGCTGAGAC 197

Qy 168 AACAAAGGACCA CGGGAGGGTAGGGAGAGGAGCAGGGATCCCCAACAC 227  
 Db 198 AACAAAGGACCA CGGGAGGGTAGGGAGAGGAGCAGGGATCCCCAACAC 257

Qy 228 CAAGTCCCCTCCAGGCTTTCGGTTCTTGCTCCATCTGGTGGCCCTCCCGCGT 287  
 Db 258 CAAGTCCCCTCCAGGCTTTCGGTTCTTGCTCCATCTGGTGGCCCTCCCGCGT 317

Qy 288 CTAGGGAGGGAAAGGCCAGGGCAGGCCAGGGAGATCTGGGACAGGACRACT 347  
 Db 318 CTAGGGAGGGAAAGGCCAGGGCAGGCCAGGGAGATCTGGGACAGGACRACT 377

Qy 348 CCCCACTGGAAAGGATCTGAAAGAATGAAGTCAAGCCCTAGAAGTAAGTGC 407  
 Db 378 CCCCACTGGAAAGGATCTGAAAGAATGAAGTCAAGCCCTAGAAGTAAGTGC 437

Qy 408 CTCTGGCTTTCCTGTTCTGTTGACTGGCCGGAGGTGTACTGCAAGACCTTGTGAGCTCCCT 467  
 Db 438 CTGCTGGCTTCTGTTGACTGGCCGGAGGTGTACTGCAAGACCTTGTGAGCTCCCT 496

Qy 468 AGCTTAAGAGTAGGATCTCTGTAAGTCACTCATCAGGTGAAGAAGCAGTGTACAG 527  
 Db 497 AGCTTAAGAGTAGGATCTCTGTAAGTCACTCATCAGGTGAAGAAGCAGTGTACAG 556

Qy 528 ATGAGAAGGAGATGCTGCTCTTGTGCGGGATGTGCTATAGATGTGGTCCACCTA 587  
 Db 557 ATGAGAAGGAGATGCTGCTCTTGTGCGGGATGTGCTATAGATGTGGTCCACCTA 616

Qy 588 ATGTCAGGACCCCTCTGGATATTTCAGGAAGAGGTAAAGCTGTGTCGGGACTTGG 647  
 Db 617 ATGTCAGGACCCCTCTGGATATTTCAGGAAGAGGTAAAGCTGTGTCGGGACTTGG 676

Qy 648 CTGAACTGCTCTAAGAGTAGGATGTGCTGAAAGTGTGAGATGGACA 707  
 Db 677 CTGAACTGCTCTAAGAGTAGGATGTGCTGAAAGTGTGAGATGGACA 736

Qy 708 GAAAAGCTGTGGAGAACCCACCTGCTAGGAACCCCTACCTGTTGGACTATAGATGTGC 767  
 Db 737 GAAAAGCTGTGGAGAACCCACCTGCTAGGAACCCCTACCTGTTGGACTATAGATGTGC 796

Qy 768 TGATGGCAGAGATGGAGGATTGGTGGATAAATCTGATGTGTCCTCATTAATTTCCTCA 827  
 Db 797 TGATGGCAGAGATGGAGGATTGGTGGATAAATCTGATGTGTCCTCATTAATTTCCTCA 856

Qy 828 TGAGGAGTACATGGCCGAGGCCAGGAAAGATAAGGAAAGACTTCTGGACCTTGTGG 887

RESULT 2  
 US-08-795-088A-1  
 Sequence 1, Application US/08795088A  
 Patent No. 6,242,569  
 GENERAL INFORMATION:  
 APPLICANT: Sui, Hong-Bing  
 APPLICANT: Goeddel, David V.  
 TITLE OF INVENTION: Regulators of Apoptosis  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Science & Technology Law Group  
 STREET: 75 Denise Drive  
 CITY: Hillsborough  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94010  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATE:  
 APPLICATION NUMBER: US/08/795,088A  
 FILING DATE:  
 CLASSIFICATION: 435

**RESULT 3**

us-08-859-167-1  
Sequence 1, Application US/08859167  
Patent No. 6037461

**GENERAL INFORMATION:**

APPLICANT: Alnemri, Emad S.  
FERNANDEZ-ALNEMRI, Teresa  
TITLE OF INVENTION: FADD-LIKE APOPTOTIC MOLECULES, METHODS OF  
USING THE SAME, AND COMPOSITIONS FOR AND METHODS  
OF MAKING THE SAME  
TITLE OF INVENTION: OF MAKING THE SAME  
NUMBER OF SEQUENCES: 17

**CORRESPONDENCE ADDRESS:**

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461ris  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103

**COMPUTER READABLE FORM:**

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: WINDOWS  
SOFTWARE: WordPerfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/859,167  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: DELCA, MARK  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: TUJ-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1750 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 413..1750

**us-08-859-167-1**

Query Match 73.5%; Score 1008.6; DB 3; Length 1750;  
Best Local Similarity 99.5%; Pred. No. 5.5e-223; Mismatches 4; Indels 1; Gaps 1;

Qy 69 CGAGTCCTCAACTAAAGGACTCCCGGAGCTAGGGACTGGGACTCGGCCCTCACAGTGA 128  
Db 1 CAGTCCTCAACTAAAGGACTCCCGGAGCTAGGGACTGGGACTCGGCCCTCACAGTGA 60

Qy 129 GTGCCGGCTATTGGACTTTGTCAGTGACAGCTGAGACACAAGGACCAAGGGAGG 188  
Db 61 GTGCCGGCTATTGGACTTTGTCAGTGACAGCTGAGACACAAGGACCAAGGGAGG 120

Qy 189 TGTAGAGAGAGCCGCAGAACGGATGCCAGCAGCCAAGTGCTGCTTCAGCTTC 248  
Db 121 TGTAGAGAGAGCCGCAGAACGGATGCCAGCAGCCAAGTGCTGCTTCAGCTTC 180

Qy 249 GGTTCTTGGCTCATCTGGTCGCTTCGGGCTTAGGGAGCAAGGGTCTGGAGG 308  
Db 181 GGTTCTTGGCTCATCTGGTCGCTTCGGGCTTAGGGAGCAAGGGTCTGGAGG 240

Qy 309 TGGCAGGGCAGGAGAGTCGGGCCGACAGGACACTCCCCACTGGAAGGGTCTG 368  
Db 241 TGGCAGGGCAGGAGAGTCGGGCCGACAGGACACTCCCCACTGGAAGGGTCTG 300

Qy 369 AAAGAAATGAAGTCAGCCCTCAGAATGAGTTGACTGCTGCTTCCTGACT 428  
Db 301 AAAGAAATGAAGTCAGCCCTCAGAATGAGTTGACTGCTGCTTCCTGACT 359

Qy 429 GGCCGGAGCTGTAATCGCAGACCCGGAGTCGGCCGAGAACCTGGCTGCTG 488  
Db 360 GGCCGGAGCTGTAATCGCAGACCCGGAGTCGGCCGAGAACCTGGCTGCTG 419

Qy 489 CTGAAGTCATCCATCAGGTTGAAAGAACGACTGATAACAGATGAGGAGATGCTCT 548  
Db 420 CTGAAGTCATCCATCAGGTTGAAAGAACGACTGATAACAGATGAGGAGATGCTCT 479

Qy 549 TTTCGGCCGGATGTTGGCTATAGTGTGGTCCGGACCTTAATGTCGGACCTTCGGATA 608  
Db 480 TTTCGGCCGGATGTTGGCTATAGTGTGGTCCGGACCTTAATGTCGGACCTTCGGATA 539

Qy 609 TTTCAGGAAAGGTTAAGTGTGGTCAAGAGGATGGAGACCCACC 668  
Db 540 TTTCAGGAAAGGTTAAGTGTGGTCAAGAGGATGGAGACCCACC 599

Qy 669 GGCAGTTGACCTCTCAAAGTATCTGGAGATGGACAGAAAGCTGTGGAGACCCACC 728  
Db 600 GGCGATTGACCTCTCAAAGTATCTGGAGATGGACAGAAAGCTGTGGAGACCCACC 659

Qy 729 TGCTCAGGAACCCCTACCTTGCGACTPATAGGTGTGGTCAAGGATTGGTGGAGG 788  
Db 660 TGCTCAGGAACCCCTACCTTGCGACTPATAGGTGTGGTCAAGGATTGGTGGAGG 719

Qy 789 ATTTCGATATCTGATGTCGCTCATTAATTTCCTCATGAGATTAGTGGCGCAG 848  
Db 720 ATTTCGATATCTGATGTCGCTCATTAATTTCCTCATGAGATTAGTGGCGCAG 779

Qy 849 GCAAGATAAGGAAAGGAAAGGTTCTGGACCTTGTGGTGAAGTGGGAAACTAAATT 908  
Db 780 GCAGTATGAGGAAAGGAAAGGTTCTGGACCTTGTGGTGAAGTGGGAAACTAAATT 839

Qy 909 TGGTGCCTCCAGATAACTGSGATTATTAGAAAAATGCCATTGGTGAATGGTGGAG 968  
Db 840 TGGTGCCTCCAGATAACTGSGATTATTAGAAAAATGCCATTGGTGAATGGTGGAG 899

Qy 969 ACCTGAGACAAATTCAGAGTACAGGACTGTTCAAGGAGCAAGTGTACAT 1028  
Db 900 ACCTGAGACAAATTCAGAGTACAGGACTGTTCAAGGAGCAAGTGTACAT 959

Qy 1029 GGAATGTTCTCCAGATAACTGSGATTATTAGAAAAATGCCATTGGTGAATGGTGGAG 1088  
Db 960 GGAATGTTCTCCAGATAACTGSGATTATTAGAAAAATGCCATTGGTGAATGGTGGAG 1019

Qy 1089 TGATAC 1095  
Db 1020 GCATAC 1026

Patent No. 6063760  
 GENERAL INFORMATION:  
 APPLICANT: Fernandez-Alnemri, Emad S.  
 TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF  
 TREATMENT OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS  
 OF INVENTION: OF MAKING THE SAME  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760 is  
 STREET: One Liberty Place, 46th floor  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIA TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: WINDOWS  
 SOFTWARE: WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/109,273  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/859,167  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Deluce, Mark  
 REGISTRATION NUMBER: 33,229  
 REFERENCE DOCKET NUMBER: TUU-  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-3100  
 TELEFAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1750 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: both  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 413..1750  
 US-09-109-273-1

Query Match 73.5%; Score 1008 6; DB 3; Length 1750;  
 Best Local Similarity 99.5%; Pred. No. 5.5e-223;  
 Matches 1022; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 69 CGACTCTCAACTAAAGGACTCCCGAGCTAGGGACTCAGCTCAACAGTGA 128  
 Db 1 CGAGTCCTCAACTAAAGGACTCCCGAGCTAGGGACTCAGCTCAACAGTGA 60  
 Qy 129 GTGCCGGCTATGGACTTTGCACTGACGTGAGCAAAAGGACAGGGAGGG 188  
 Db 61 GTGCCGGCTATGGACTTTGCACTGACGTGAGCAAAAGGACAGGGAGGG 120  
 Qy 189 TGAGGAGAGAGGCGGAGACGGATCCCCAACCAAGTCCAGGCTTCAGGGACTCAGCTCAACAGTGA 308  
 Db 121 TGAGGAGAGAGGCGGAGACGGATCCCCAACCAAGTCCAGGCTTCAGGGACTCAGCTCAACAGTGA 180  
 Qy 249 GGTTTCCTTGCTCCATCTGGTGGCTCCGGCTTCCAGGCTTCAGGGACTCAGCTCAACAGTGA 308  
 Db 181 GGTTTCCTTGCTCCATCTGGTGGCTTCCGGCTTCCAGGCTTCAGGGACTCAGCTCAACAGTGA 240  
 Qy 309 TGGCAGGGAGAGGAGCTGGCGGAGACGGGACTCCCACTGAGAAGGGATTCTG 368  
 Db 241 TGGCAGGGAGAGGAGCTGGCGGAGACGGGACTCCCACTGAGAAGGGATTCTG 300  
 Qy 369 AAAGAAATGAAGTCAGCCCTAGAAATGAAGTGTGACTGCCTGCGTTCCTGTTGACT 428  
 Db 301 AAAGAAATGAAGTCAGCCCTAGAAATGAAGTGTGACTGCCTGCGTTCCTGTTGACT 359

Qy 429 GGCCGGAGCTGCTACTCCAAGACCCTTGTGAGCTCCCTAGTCTAAGACTGGATGTCG 488  
 Db 360 GGCCGGAGCTGCTACTCCAAGACCCTTGTGAGCTCCCTAGTCTAAGACTGGATGTCG 419  
 Qy 489 CTGAAGTCATCCATCAGTGAAGGAGCACTGATCACATGAGAAGGAGATGCGCTCT 548  
 Db 420 CTGAAGTCATCCATCAGTGAAGGAGCACTGATCACATGAGAAGGAGATGCGCTCT 479  
 Qy 549 TTGTTGCGGGATGTTGCTPATAGATGGTCCACCTAATGTCAGGACCTTCGGATA 608  
 Db 480 TTGTTGCGGGATGTTGCTPATAGATGGTCCACCTAATGTCAGGACCTTCGGATA 539  
 Qy 609 TTTCACGGAAAGGAAAGCTTGGGACTCTGGCTGAACCTTCAGAGTGA 668  
 Db 540 TTTCACGGAAAGGAAAGCTTGGGACTCTGGCTGAACCTTCAGAGTGA 599  
 Qy 669 GGCAGATTGACTGCTCAAAGGTATCTTGAAGATGGACAGAAAAGCTGTTGGAGACCCACC 728  
 Db 600 GGCAGATTGACCTGCTCAAACGTAATTTGAGATGGACAGATGGTGGAGACCCACC 659  
 Qy 729 TGCTCAGGAACCTCACCTGTTGGACTATAGCTGCTGATGGCAGAGATTGTGAGG 788  
 Db 660 TGCTCAGGAACCTCACCTGTTGGACTATAGCTGCTGATGGCAGAGATTGTGAGG 719  
 Qy 789 ATTTGATAAAATCTGATGTPCTCATTAATTCTCATGAAGGATTACATGGCCGAG 848  
 Db 720 ATTTGATAAAATCTGATGTPCTCATTAATTCTCATGAAGGATTACATGGCCGAG 779  
 Qy 849 GCAAGATAAGGAAAGGAAAGGTCTTGACCTTGTGGTTGAGTTGGAGAAACTTAATT 908  
 Db 780 GCAAGATAAGGAAAGGAAAGGTCTTGACCTTGTGGTTGAGTTGGAGAAACTTAATT 839  
 Qy 909 TGGTTCCTCCAGATAACTGGATTAGAAAAATGCTPAAAGGACATTCACAGATAAG 968  
 Db 840 TGGTTCCTCCAGATAACTGGATTAGAAAAATGCTPAAAGGACATTCACAGATAAG 899  
 Qy 969 ACCTGAGACAAAATCAGAATCAAGTCAAGGACAGGTCTTCAAGGACAGGTACA 1028  
 Db 900 ACCTGAGACAAAATCAGAATCAAGTCAAGGACAGGTCTTCAAGGACAGGTACA 959  
 Qy 1029 GGAATTTCTCAGAGGCAATCCAAAGGCTCAAGGATCCCTCAAATAACTTCAGGA 1088  
 Db 960 GGAATTTCTCAGAGGCAATCCAAAGGCTCAAGGATCCCTCAAATAACTTCAGGA 1019  
 Qy 1089 TGATAC 1095  
 Db 1020 GCATAC 1026

RESULT 5  
 US-09-276-993-1  
 Sequence 1, Application US/09276993  
 ; Patent No. 60637601  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alnemri, Emad S.  
 ; APPLICANT: Fernandez-Alnemri, Teresa  
 ; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF  
 ; TREATMENT OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS  
 ; OF INVENTION: OF MAKING THE SAME  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801ris  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: WINDOWS  
 ; SOFTWARE: WordPerfect  
 ; COMPUTER READABLE FORM:  
 ; ZIP: 19103  
 ; CITY: Philadelphia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ;

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/276,993  
 FILING DATE: 08/09/2003  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/859,167  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DELUCA, Mark  
 REGISTRATION NUMBER: 33,229  
 REFILE/DOCKET NUMBER: TUDU-  
 TELECOMMUNICATION INFORMATION:  
 PHONE: (215) 568-3100  
 TELEFAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1750 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: both  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 413..1750  
 US-09-276-993-1

Query Match      73.5%;    Score 1008.6;    DB 4;    Length 1750;  
 Best Local Similarity 99.5%;    Pred. No. 5.5e-223;  
 Matches 1022;    Conservative 0;    Mismatches 4;    Indels 1;    Gaps 1;

Qy 69 CGAGTCCTCAACTAAAGGAATCCCGGAACTTGGGTGGGAACTCGGCCTCACAGTGA 128  
 Db 1 CGAGTCCTCAACTAAAGGAATCCCGGAACTTGGGTGGGAACTCGGCCTCACAGTGA 60

Qy 129 GTGCCGGCTCATGGACTTTGCCAGTGACGTGACACAAGAACGACACGGGAGGG 188  
 Db 61 GTGCCGGCTCATGGACTTTGCCAGTGACGTGACACAAGAACGACACGGGAGGG 120

Qy 189 TGTAAGGAGAAGGCCGGACGGATGCCCAAGCAGAACGATGCCCAAGTCCAGGCTTC 248  
 Db 121 TGTAAGGAGAAGGCCGGACGGATGCCCAAGCAGAACGATGCCCAAGTCCAGGCTTC 180

Qy 249 GTTTCTTGCTCCATCTGGTGGCCCTCCGGCTTAGGGAGGGTGG 308  
 Db 181 GTTTCTTGCTCCATCTGGTGGCCCTCCGGCTTAGGGAGGGTGG 240

Qy 309 TGGCAGGGCAGGAGTCCGGCGAACGGAGCAACTCCCCACTGGAAAGGATTCTG 368  
 Db 241 TGGCAGGGCAGGAGTCCGGCGAACGGAGCAACTCCCCACTGGAAAGGATTCTG 300

Qy 369 AAAGAAATGAAGTCASCCCTCGAAATGAACTTGTACTGGCTGCTGCTGTGACT 428  
 Db 301 AAAGAAATGAAGTCAGCTCAGAAATGAAGTGTACTGGCTGCTGCTGTGACT 359

Qy 429 GGCCCGGAGGAGTACGCAACCCPTGTGACTCTTAAGATPAGGATGTCG 488  
 Db 360 GGCCCGGAGGAGTACGCAACCCPTGTGACTCTTAAGATPAGGATGTCG 419

Qy 489 CTGAAGTCATCCCACGGATGTCATAGATGTCAGGATGAGAAGGAGACTGTGCTCT 548  
 Db 420 CTGAAGTCATCCCACGGATGTCATAGATGTCAGGATGAGAAGGAGACTGTGCTCT 479

Qy 549 TTTCGCGCGSATGTCATAGATGTCAGGATGAGAAGGAGACTGTGCTCT 608  
 Db 480 TTTCGCGCGSATGTCATAGATGTCAGGATGTCAGGATGTCAGGATGTCAGGATGTC 539

Qy 609 TTTCAGGGAAAGAGTAAGCTGTGCTGCGGACTGTGTCAGTCAAGATG 668  
 Db 540 TTTCAGGGAAAGAGTAAGCTGTGCTGCGGACTGTGTCAGTCAAGATG 599

Qy 669 GCGGATTTGACCTGCTCAACGTTCTGAGATGGACAGAAAAGCTGTGGAGACCACC 728  
 Db 600 GCGGATTTGACCTGCTCAACGTTCTGAGATGGACAGAAAAGCTGTGGAGACCACC 659

Best Local Similarity 73.7%; Pred. No. 2.6e-09;  
 Matches 101; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

RESULT 7  
 US-08-345-196B-12  
 ; Sequence 12, Application US/08545196B  
 ; Patent No. 6080577  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: MUNNICH, ARNOLD  
 ; TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE  
 ; NUMBER OF INVENTION: FOR SPINAL MUSCULAR ATROPHY  
 ; NUMBER OF SEQUENCES: 65  
 ; CORRESPONDENCE ADDRESS:  
 ;  
 ; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP  
 ; STREET: PO BOX 747  
 ; CITY: FALLS CHURCH  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22040-0747  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, version #1.30  
 ; CURRENT APPLICATION DATA:  
 ;  
 ; APPLICATION NUMBER: US/08/545,196B  
 ; FILING DATE: 19-OCT-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: FARCI, C. J.  
 ; REGISTRATION NUMBER: 32,350  
 ; REFERENCE/DOCKET NUMBER: 2121-110P  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703) 205-8000  
 ; TELEFAX: (703) 205-8050  
 ; INFORMATION FOR SEQ ID NO: 12:  
 ;  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1582 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-08-345-196B-12

Query Match Similarity 73.7%; Pred. No. 2.6e-09;  
 Matches 101; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

RESULT 8  
 US-08-909-965C-7  
 ; Sequence 7, Application US/08909965C  
 ; Patent No. 5936078  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Kuga Tetsuro  
 ; APPLICANT: Nakagawa Satoshi  
 ; APPLICANT: Sakaki Yoshiyuki  
 ; APPLICANT: Zhao Nanding  
 ; APPLICANT: Hashida Hideji  
 ; TITLE OF INVENTION: NOVEL DNA, NOVEL POLYPEPTIDE  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FITZPATRICK, CELLA, HARPER AND SCINTO  
 ; STREET: 277 Park Avenue  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10172-0194  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ;  
 ; APPLICATION NUMBER: US/08/909,965C  
 ; FILING DATE: August 12, 1997  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ;  
 ; APPLICATION NUMBER: JP 322745/95  
 ; APPLICATION NUMBER: PC7/JP96/03630  
 ; FILING DATE: 12-No. 5916078-1995  
 ; FILING DATE: 12-Dec-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Lawrence S. Perry  
 ; REGISTRATION NUMBER: 31,865  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-758-2400  
 ; TELEFAX: 212-758-2982  
 ; TELEX: 236262  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ;  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3527 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA to mRNA  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: human  
 ; IMMEDIATE SOURCE:  
 ; CLONE: F998  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 140 to 1084  
 ; IDENTIFICATION METHOD: by experiment  
 ; US-08-909-965C-7

Query Match Similarity 5.7%; Score 78.4%; DB 2; Length 3527;  
 Best Local Similarity 81.2%; Pred. No. 6e-09;  
 Matches 91; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1237 TGGCTGTAGTGTAGTGTAGCTTCCAACTCTTGTACTACTAATATGCTATAAAATAAA 1296  
 Db 1415 TGGCTGTAGTGTAGCTTCTATCTCTATGTTAAAGTGTATAATATAAA 1474  
 Qy 1289 TATCCGTGTACTCTTAATATGCTATAATGTTAAAGTGTATAATATAAA 1356  
 Db 1475 TATTAATTCTTTPAATATGCTATAATGTTAAAGTGTATAATATAAA 1534  
 Qy 1357 AAAAAAAA 1373  
 Db 1535 AAAAAAAA 1551  
 Qy 1322 AAAAAAAA 1373  
 Db 3468 AAAAAAAA 3519

RESULT 9  
US-09-372-422A-19  
; Sequence 19, Application US/09372422A  
; Patent No. 6313375  
; GENERAL INFORMATION:  
; APPLICANT: Rudolf Jung  
; APPLICANT: Francois Barrieu  
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof  
; FILE REFERENCE: 0919  
; CURRENT FILING DATE: 1999-08-11  
; PRIOR APPLICATION NUMBER: US 60/098,692  
; PRIOR FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 1454  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (224) ... (1112)

RESULT 10  
US-08-821-994-63  
; Sequence 63, Application US/08821994A  
; Patent No. 6228643  
; GENERAL INFORMATION:  
; APPLICANT: Greenland, Andrew J  
; APPLICANT: Thomas, Didier RP  
; APPLICANT: Jepson, Ian  
; TITLE OF INVENTION: Promoters  
; FILE REFERENCE: PPD 50108  
; CURRENT APPLICATION NUMBER: US/08/821 994A  
; CURRENT FILING DATE: 1997-03-22  
; EARLIER APPLICATION NUMBER: PCT/GB97/00729  
; EARLIER FILING DATE: 1997-03-18  
; EARLIER APPLICATION NUMBER: GB 9606062.9  
; EARLIER FILING DATE: 1996-03-22  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 63  
; LENGTH: 1441  
; TYPE: DNA  
; ORGANISM: Brassica napus

RESULT 11  
US-09-149-476-24  
; Sequence 24, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Human Secreted Proteins  
; FILE REFERENCE: PZ00221  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,583  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,500  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,587  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,492  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,598  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,613  
; EARLIER FILING DATE: 1997-05-23

Query Match 5.6%; Score 76.8; DB 4; Length 1441;  
Best Local Similarity 62.5%; Pred. No. 1e-08;  
Matches 120; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Qy 1181 AATGATTAAATCGTTTCATTTCTAAATGTTATAATGTTAGCCCTTCTGTGTC 1240  
Db 1250 ATGGTACCCATAGGGATTAATCTGTATAATCATTCTATGTGCTAACAT 1309



QY 1116 ATCTGAAATTCTGGAAATTGGTCCATGTGATAACATGGAACTGCCCTACTTAATCA 1175  
 Db 2059 ACCGATTTATGAAACATGAGACGGATATAGCCCTAACGATATTTG 2118  
 Qy 1176 TTCTGAATGATTAATCGTTCATTTCTAAATGTTAGCCTTCT 1235  
 Db 2119 GACTAAARATACATTTAACCTGCTCTGCCTAGTACCATGCTAGTCCAATGA 2178

RESULT 13  
 US-09-027-137-2 ; Sequence 2, Application US/09/027137  
 ; Patent No. 6013450 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Corley, Neil C.  
 ; APPLICANT: Yue, Henry  
 ; TITLE OF INVENTION: CAF1-RELATED PROTEIN  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; STREET: 3174 Porter Dr.  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304

Db 2179 TTATTCCTGTGACAACTGATGCTGTTATTATTAATTCAGAGTGA 2238

Qy 1296 ATATCCTTGTACTCTTAAAAA 1355  
 Db 2239 AAAA 1373  
 Qy 1356 AAAA 1373  
 Db 2299 AAAA 2316

RESULT 12  
 US-09-013-810-1 ; Sequence 1, Application US/09/013810  
 ; Patent No. 6197531 ; GENERAL INFORMATION:  
 ; APPLICANT: Busfield, Samantha J.  
 ; TITLE OF INVENTION: NO. 6197551el TANGO 80 Molecules and Uses Thereof  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 ; STREET: 28 State Street  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02109

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/013, 810  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Amy E. Mandragouras  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: MEI-010  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 742-4214  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 746 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 135..428

Query Match 5.4%; Score 74.8; DB 4; Length 746;  
 Best Local Similarity 77.1%; Pred. NO. 2.3e-08; Indels 0; Gaps 0;  
 Matches 91; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

US-09-013-810-1 ; Query Match 5.4%; Score 74.8; DB 4; Length 746;  
 Best Local Similarity 77.1%; Pred. NO. 2.3e-08; Indels 0; Gaps 0;  
 Matches 91; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 1256 TTCCGAATCTTTGTACTACTAAATCTATAATCCTGTACTCTTAA 1315  
 Db 2544 AAAA 2558

Db 611 TTACTGTTGGTTTACAGGAGTGAATTCTTAAATAATCATTATCATAAAA 670  
 Qy 1316 AAAA 1373  
 Db 671 AAAA 1373

RESULT 14



GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using SW model

Run on: April 12, 2003, 22:29:49 : Search time 21.2268 Seconds  
(without alignments)  
1382.463 Million cell updates/sec

Title: US-09-380-546A-2  
Perfect score: 2473  
Sequence: 1 MSAEVHQVEEALDTDEKEM. .... EKYYVNLQHTLRLKKLILSYT 480

Scoring table: BL05UN62  
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 2488112

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:  
 1: /cgn2\_6/pctodata/2/pubpaa/us08\_new\_pub.pep:  
 2: /cgn2\_6/pctodata/2/pubpaa/bct\_new\_pub.pep:  
 3: /cgn2\_6/pctodata/2/pubpaa/us06\_new\_pub.pep:  
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 10: /cgn2\_6/pctodata/2/pubpaa/us09\_pubcomb.pep:  
 11: /cgn2\_6/pctodata/2/pubpaa/us10\_new\_pub.pep:  
 12: /cgn2\_6/pctodata/2/pubpaa/us10\_pubcomb.pep:  
 13: /cgn2\_6/pctodata/2/pubpaa/us60\_new\_pub.pep:  
 14: /cgn2\_6/pctodata/2/pubpaa/us60\_pubcomb.pep:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	2468	99.8	480	10 US-09-061-270-2	Sequence 2, Appli
2	2468	99.8	480	10 US-09-061-194-11	Sequence 11, Appli
3	2468	99.8	480	10 US-09-061-194-17	Sequence 17, Appli
4	1580	63.9	481	10 US-09-061-194-12	Sequence 12, Appli
5	1580	63.9	481	10 US-09-061-194-19	Sequence 19, Appli
6	1568.5	63.4	484	9 US-10-005-921-2	Sequence 2, Appli
7	1007	40.7	221	10 US-09-061-194-15	Sequence 15, Appli
8	1007	40.7	221	10 US-09-061-194-22	Sequence 22, Appli
9	465	18.8	93	10 US-09-064-761-36370	Sequence 36370, A
10	410	16.6	479	10 US-09-061-194-20	Sequence 20, Appli
11	389	15.7	76	10 US-09-064-761-35073	Sequence 35073, A
12	381.5	15.4	496	10 US-09-052-768-4	Sequence 4, Appli
13	370.5	15.0	476	10 US-09-054-697-27	Sequence 27, Appli
14	323.5	13.1	521	10 US-09-056-834A-2	Sequence 2, Appli
15	323.5	13.1	571	10 US-09-056-834A-2	Sequence 21, Appli
16	318.5	12.9	479	10 US-09-052-768-2	Sequence 2, Appli
17	318.5	12.9	479	10 US-09-054-697-33	Sequence 33, Appli
18	248	10.0	182	10 US-09-061-194-24	Sequence 24, Appli
19	246.5	10.0	286	10 US-09-062-915-1	Sequence 1, Appli

## ALIGNMENTS

RESULT 1  
US-09-861-270-2  
; Patent No. US20020052474A1  
; GENERAL INFORMATION:  
; APPLICANT: Sui, Hong-Bing  
; GOEDDEL, David V.  
; TITLE OF INVENTION: Regulators of Apoptosis  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Science & Technology Law Group  
; STREET: 75 Denise Drive  
; CITY: Hillsborough  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94010  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/861-270  
FILING DATE: 18-May-2001  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
ATTORNEY/AGENT INFORMATION:  
NAME: Osman, Richard A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 480 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 99.8%; Score 2468; DB 10; Length 480;  
 Best Local Similarity 99.8%; Pred. No. 2e-199;  
 Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSAEVTHQEAEALDTDEKEMLLFLCRDVKAVETHLLRNPVLSYDVRVMAEIGEDLDKSDVSSLJFLMKDM 60  
 Db 1 MSAEVTHQEAEALDTDEKEMLLFLCRDVKAVETHLLRNPVLSYDVRVMAEIGEDLDKSDVSSLJFLMKDM 60

Qy 61 RVRRFDLKLKRILKMDRKAVETHLLRNPVLSYDVRVMAEIGEDLDKSDVSSLJFLMKDM 120  
 Db 61 RVRRFDLKLKRILKMDRKAVETHLLRNPVLSYDVRVMAEIGEDLDKSDVSSLJFLMKDM 120

Qy 61 RVRRFDLKLKRILKMDRKAVETHLLRNPVLSYDVRVMAEIGEDLDKSDVSSLJFLMKDM 120  
 Db 61 RVRRFDLKLKRILKMDRKAVETHLLRNPVLSYDVRVMAEIGEDLDKSDVSSLJFLMKDM 120

Qy 121 GRGKISKEKSFLDVVELEKLNLYAPDQLDLIEKCLKNIRDLKTKIQKYQSVCAGT 180  
 Db 121 GRGKISKEKSFLDVVELEKLNLYAPDQLDLIEKCLKNIRDLKTKIQKYQSVCAGT 180

Qy 181 SYRNVLQRAIQSLKPSNFRQHNGRSKEQRLKEQLGAAQEPVKKS1QESEARFLPOSIP 240  
 Db 181 SYRNVLQRAIQSLKPSNFRQHNGRSKEQRLKEQLGAAQEPVKKS1QESEARFLPOSIP 240

Qy 181 SYRNVLQRAIQSLKPSNFRQHNGRSKEQRLKEQLGAAQEPVKKS1QESEARFLPOSIP 240  
 Db 181 SYRNVLQRAIQSLKPSNFRQHNGRSKEQRLKEQLGAAQEPVKKS1QESEARFLPOSIP 240

Qy 241 EERYKMKSPPLGICLIDIGINETELLRTDFTSLGYEVOKFHLHSMHGISQTLGOFACMP 300  
 Db 241 EERYKMKSPPLGICLIDIGINETELLRTDFTSLGYEVOKFHLHSMHGISQTLGOFACMP 300

Qy 301 EHRYDYSFCVLYSRRGGSSCVYDQTHSGPLHIIHRMFDGSCPYLAKGPKMFIONY 360  
 Db 301 EHRYDYSFCVLYSRRGGSSCVYDQTHSGPLHIIHRMFDGSCPYLAKGPKMFIONY 360

Qy 361 VVSEGQLENSSLLEVDPAMKNAVEFKAQKRGCLCTVREADFFWSLCTADMSLLEQSHSSP 420  
 Db 361 VVSEGQLENSSLLEVDPAMKNAVEFKAQKRGCLCTVREADFFWSLCTADMSLLEQSHSSP 420

Qy 421 SLYLOCLSOKLROERKRPLLDLHIELNGMYDWNRSYSAKEKYVWLOHTLRKKLILSYT 480  
 Db 361 VVSEGQLENSSLLEVDPAMKNAVEFKAQKRGCLCTVREADFFWSLCTADMSLLEQSHSSP 420

Qy 421 SLYLOCLSOKLROERKRPLLDLHIELNGMYDWNRSYSAKEKYVWLOHTLRKKLILSYT 480  
 Db 421 SLYLOCLSOKLROERKRPLLDLHIELNGMYDWNRSYSAKEKYVWLOHTLRKKLILSYT 480

RESULT 3

US-09-410-194-17

Sequence 17, Application US/09410194

; Patent No. US20020095030A1

; GENERAL INFORMATION:

; APPLICANT: Tschopp, Jurg

; APPLICANT: Thome, Margot

; APPLICANT: Irmler, Marten

; APPLICANT: Hahne, Michael

; APPLICANT: Schroter, Michael

; APPLICANT: Schneider, Pascal

; APPLICANT: Bodmer, Jean-Luc

; APPLICANT: Steiner, Veronique

; APPLICANT: Rimoldi, Donata

; APPLICANT: Hofmann, Kay

; APPLICANT: French, E. Lars

; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS

; FILE REFERENCE: 11141-002001

; CURRENT APPLICATION NUMBER: US/09/410,194

; CURRENT FILING DATE: 1999-09-30

; PRIORITY NUMBER: PCT/EP98/01857

; PRIOR FILING DATE: 1998-03-31

; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2

; PRIOR FILING DATE: 1997-04-01

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 11

; LENGTH: 480

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-410-194-17

; Query Match 99.8%; Score 2468; DB 10; Length 480;

; Best Local Similarity 99.8%; Pred. No. 2e-199; Matches 479; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



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Db	RVRFDLKLRLKMKDRAVETHLRNPFLSDYRVLMAIEGEDLDSVSSLFLMLKDM	120	Db	186	A-RSMNTLQAASPLPLSIK--YNSRLQNSRSKERFVEVDRDQSQTFLVTSIQEGSAFLP	29
Qy	61 RVRFDLKLRLKMKDRAVETHLRNPFLSDYRVLMAIEGEDLDSVSSLFLMLKDM	120	Qy	237	QSIPERFYKMKSKPGLIGCLIDCIGNETELLRDPTTSLSGYEVQRFLHLSMHGISQILQF	29
Db	RVRFDLKLRLKMKDRAVETHLRNPFLSDYRVLMAIEGEDLDSVSSLFLMLKDM	125	Db	242	PHIREBETYRQSKPPGICLIDCNDTYLOETTSLSGLHFIOLFLFPKSHDITDVLVRRY	301
Qy	66 RVRFDLKLRLKMKDRAVETHLRNPFLSDYRVLMAIEGEDLDSVSSLFLMLKDM	125	Qy	297	ACMPBEPHDYDFSFVCYLVLSRGGSOSVSYGVDOHTSGPLHHIIRRMMFGDSCPYLAGPKMF	416
Db	GRGKISKEKSFSDLVYVLEKLNLVAPPDLLEKCLKNHRDLKTIQKYSVQAGT	180	Db	302	ASMAQHODYQDSEACFLVSLGGQSOMGRDQHSGSLDHVNMTGDTCPSLRGPKLFF	420
Qy	121 GRGKISKEKSFSDLVYVLEKLNLVAPPDLLEKCLKNHRDLKTIQKYSVQAGT	180	Qy	297	ACMPBEPHDYDFSFVCYLVLSRGGSOSVSYGVDOHTSGPLHHIIRRMMFGDSCPYLAGPKMF	416
Db	GRGKIAKDKSFSDLVYVLEKLNLVAPPDLLEKCLKNHRDLKTIQKYSVQAGT	184	Db	302	ASMAQHODYQDSEACFLVSLGGQSOMGRDQHSGSLDHVNMTGDTCPSLRGPKLFF	420
Qy	181 SYRNVLQAAIK-SLKDPSPNNFRHLNGRSKEORLKEOLGAQOEPVKSIOSSEAFLPQ	239	Db	302	ASMAQHODYQDSEACFLVSLGGQSOMGRDQHSGSLDHVNMTGDTCPSLRGPKLFF	420
Db	185 SMNTLQAASPLPLSIK--YNSRLQNSRSKEPRFEVDRDQSQTFLVTSIQEGAFLPHI	241	Qy	357	IQNVYVSEGOLNSSLLEVGPAMMNLVEKAQKRLCTVREADFWSLCTADMSPLEQS	480
Qy	240 PEERYKMKSKPGLIGCLIDCIGNETELLRDPTTSLSGYEVQRFLHLSMHGISQILQFACM	299	Db	362	IQNYESLGSOLEDSS-LEVDGPSIKVNDSKPLQOPRCHTPHEADFWSLCTADVSHELEKP	420
Db	REBETYRQSKPPGICLIDCNDTYLOETTSLSGLHFIOLFLFPKSHDITDVLVRRYAS	301	Qy	417	HSSPPLYLOCLSOKLQRERKRPLLDLHIELNGNMWDNSRVSAYAKEKYYVWQHTLRKKLI	476
Qy	300 PEHYDPSFVCYLVLSRGGSOSVSYGVDOHTSGPLHHIIRRMMFGDSCPYLAGPKMFPTQ	359	Db	421	SSSSAVYLOKLSQLQGRRPLPVLDHVELMDKVYAWNNSVSSKREKYSLSLQHTLRKKLI	480
Db	302 AQHODYDSEACFLVSLGGQSOMGRDQHSGSLDHVNMTGDTCPSLRGPKLFFTQ	361	Qy	477	LSTY 480	
Qy	360 YVSEGOLENSSLLEVGPAMMNLVEKAQKRLCTVREADFWSLCTADMSPLEQS	419	Db	481	LAPT 484	
Db	362 YESLGSOLEDSS-LEVDGPSIKVNDSKPLQOPRCHTPHEADFWSLCTADVSHELEKPSS	420				
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				US-09-410-194-15		
				; Sequence 15, Application US/09410194		
				; Patent No. US20000951030A1		
				; GENERAL INFORMATION:		
				; APPLICANT: Tschopp, Jurg		
				; APPLICANT: Thome, Margot		
				; APPLICANT: Burns, Kimberly		
				; APPLICANT: Irmler, Marten		
				; APPLICANT: Hahne, Michael		
				; APPLICANT: Schroter, Michael		
				; APPLICANT: Schneider, Pascal		
				; APPLICANT: Bodmer, Jean-Luc		
				; APPLICANT: Steiner, Veronique		
				; APPLICANT: Rimoldi, Donata		
				; APPLICANT: Hofmann, Kay		
				; APPLICANT: French, E. Lars		
				; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS		
				; FILE REFERENCE: 11141-002001		
				; CURRENT APPLICATION NUMBER: US/09/410,194		
				; CURRENT FILING DATE: 1999-09-30		
				; PRIOR APPLICATION NUMBER: PCT/EP98/01857		
				; PRIOR FILING DATE: 1998-03-31		
				; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2		
				; PRIOR FILING DATE: 1997-04-01		
				; NUMBER OF SEQ ID NOS: 27		
				; SOFTWARE: FastSeq for Windows Version 4.0		
				; SEQ ID NO 15		
				; LENGTH: 221		
				; TYPE: PRT		
				; ORGANISM: Homo sapiens		
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				Mismatches 0; Indels 0; Gaps		
				Matches 202; Conservative 1; Mismatches 0;		
				Best Local Similarity 99.5%; Pred. No. 4.3e-77;		
				Mismatches 0; Indels 0; Gaps		
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				Best Local Similarity 99.5%; Pred. No. 4.3e-77;		
				Mismatches 0; Indels 0; Gaps		
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				Mismatches 0; Indels 0; Gaps		
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				Best Local Similarity 99.5%; Pred. No. 4.3e-77;		
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				Mismatches 0; Indels 0; Gaps		
				Matches 202; Conservative 1; Mismatches 0;		
				Best Local Similarity 99.5%; Pred. No. 4.3e-77;		
				Mismatches 0; Indels 0; Gaps		
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				Mismatches 0; Indels 0; Gaps		
				Matches 202; Conservative 1; Mismatches 0;		
				Best Local Similarity 99.5%; Pred. No. 4.3e-77;		
				Mismatches 0; Indels 0; Gaps		
				Matches 202; Conservative 1; Mismatches 0;		
				Best Local Similarity 99.5%; Pred. No. 4.3e-77;		
				Mismatches 0; Indels 0; Gaps		
				Matches 202; Conservative 1; Mismatches 0;		
				Best Local Similarity 99.5%; Pred. No. 4.3e-77;		
				Mismatches 0; Indels 0; Gaps		
				Matches 202; Conservative 1; Mismatches 0;		
				Best Local Similarity 99.5%; Pred. No. 4.3e-77;		
				Mismatches 0; Indels 0; Gaps		
				Matches 202; Conservative 1; Mismatches 0;		
				Best Local Similarity 99.5%; Pred. No. 4.3e-77;		
				Mismatches 0; Indels 0; Gaps		
				Matches 202; Conservative 1; Mismatches 0;		
				Best Local Similarity 99.5%; Pred. No. 4.3e-77;		
				Mismatches 0; Indels 0; Gaps		
			</td			

RESULT 8 CURRENT APPLICATION NUMBER: US/09/864,761  
 CURRENT FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: US 60/180,312  
 PRIOR FILING DATE: 2000-02-04  
 PRIOR APPLICATION NUMBER: US 60/207,456  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: US 09/632,366  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: GB 24263,6  
 PRIOR FILING DATE: 2000-10-04  
 PRIOR APPLICATION NUMBER: US 60/236,359  
 PRIOR FILING DATE: 2000-09-27  
 PRIOR APPLICATION NUMBER: PCT/US01/00666  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00664  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00669  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00665  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00663  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00662  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00661  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00670  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: US 60/234,687  
 PRIOR FILING DATE: 2000-09-21  
 PRIOR APPLICATION NUMBER: US 09/608,408  
 PRIOR FILING DATE: 2000-06-30  
 PRIOR APPLICATION NUMBER: US 09/774,203  
 PRIOR FILING DATE: 2001-01-29  
 NUMBER OF SEQ ID NOS: 49117  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 22  
 LENGTH: 221  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-410-194-22

Query Match 40.7%; Score 1007; DB 10; Length 221;  
 Best Local Similarity 99.5%; Pred. No. 4.3e-77;  
 Matches 202; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MSAEVTHOEEALDTEKMLFLCRDVADVVPPNVRDLDILRERGLSYGVGDLAELLY 60  
 1 MSAEVTHOEEALDTEKMLFLCRDVADVVPPNVRDLDILRERGLSYGVGDLAELLY 60

Db 1 MSAEVTHOEEALDTEKMLFLCRDVADVVPPNVRDLDILRERGLSYGVGDLAELLY 60

Qy 61 RVRRFDLKRILKMDRKAVETHLLRNPHVSDYRVLMAIGEDLDKSDVSSFLMKDYM 120  
 61 RVRRFDLKRILKMDRKAVETHLLRNPHVSDYRVLMAIGEDLDKSDVSSFLMKDYM 120

Db 121 GRGKISKERSFLDVLEELKLNVAPDQDLERCLKLNTHRIDLTKTOKYKOSVQGAGT 180  
 121 GRGKISKERSFLDVLEELKLNVAPDQDLERCLKLNTHRIDLTKTOKYKOSVQGAGT 180

Qy 181 SYRVLQAAIQKSLSKDPSSNFRM 203  
 181 SYRVLQAAIQKSLSKDPSSNFRM 203

Db 181 SYRVLQAAIQKSLSKDPSSNFRM 203

RESULT 9 CURRENT APPLICATION NUMBER: US/09/864,761  
 CURRENT FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: US 60/180,312  
 PRIOR FILING DATE: 2000-02-04  
 PRIOR APPLICATION NUMBER: PCT/US01/00666  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00663  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00662  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00661  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00670  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: US 60/234,687  
 NUMBER OF SEQ ID NOS: 49117  
 SOFTWARE: Annotrax Sequence Listing Engine vers. 1.1  
 SEQ ID NO 36370  
 LENGTH: 93  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: MAP TO AC007272.2  
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5  
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8  
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2  
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1  
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.9  
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3  
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.5  
 OTHER INFORMATION: EXPRESSED IN BT74, SIGNAL = 2.6  
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5  
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2  
 OTHER INFORMATION: SWISSPROT HIT: Q66674, EVALUE 3.00e-04  
 OTHER INFORMATION: SWISSPROT HIT: EST\_HUMAN HIT: W23795.1, EVALUE 2.00e-46  
 US-09-410-194-22

Query Match 18.8%; Score 465; DB 10; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-32;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSAEVTHOEEALDTEKMLFLCRDVADVVPPNVRDLDILRERGLSYGVGDLAELLY 60

Qy 1 MSAEVTHOEEALDTEKMLFLCRDVADVVPPNVRDLDILRERGLSYGVGDLAELLY 60

Db 1 MSAEVTHOEEALDTEKMLFLCRDVADVVPPNVRDLDILRERGLSYGVGDLAELLY 60

Qy 61 RVRRFDLKRILKMDRKAVETHLLRNPHVSDYRVLMAIGEDLDKSDVSSFLMKDYM 120

Db 61 RVRRFDLKRILKMDRKAVETHLLRNPHVSDYRVLMAIGEDLDKSDVSSFLMKDYM 120

Qy 121 GRGKISKERSFLDVLEELKLNVAPDQDLERCLKLNTHRIDLTKTOKYKOSVQGAGT 180

Db 121 GRGKISKERSFLDVLEELKLNVAPDQDLERCLKLNTHRIDLTKTOKYKOSVQGAGT 180

Qy 181 SYRVLQAAIQKSLSKDPSSNFRM 203

Db 181 SYRVLQAAIQKSLSKDPSSNFRM 203

RESULT 9 CURRENT APPLICATION NUMBER: US/09/864,761  
 CURRENT FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: US 60/180,312  
 PRIOR FILING DATE: 2000-02-04  
 PRIOR APPLICATION NUMBER: PCT/US01/00666  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00663  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00662  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00661  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00670  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: US 60/234,687  
 NUMBER OF SEQ ID NOS: 49117  
 SOFTWARE: Annotrax Sequence Listing Engine vers. 1.1  
 SEQ ID NO 36370  
 LENGTH: 93  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: MAP TO AC007272.2  
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5  
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8  
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2  
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1  
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.9  
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3  
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.5  
 OTHER INFORMATION: EXPRESSED IN BT74, SIGNAL = 2.6  
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5  
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2  
 OTHER INFORMATION: SWISSPROT HIT: Q66674, EVALUE 3.00e-04  
 OTHER INFORMATION: SWISSPROT HIT: EST\_HUMAN HIT: W23795.1, EVALUE 2.00e-46  
 US-09-410-194-22

Query Match 18.8%; Score 465; DB 10; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-32;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSAEVTHOEEALDTEKMLFLCRDVADVVPPNVRDLDILRERGLSYGVGDLAELLY 60

Qy 1 MSAEVTHOEEALDTEKMLFLCRDVADVVPPNVRDLDILRERGLSYGVGDLAELLY 60

Db 1 MSAEVTHOEEALDTEKMLFLCRDVADVVPPNVRDLDILRERGLSYGVGDLAELLY 60

Qy 61 RVRRFDLKRILKMDRKAVETHLLRNPHVSDYRVLMAIGEDLDKSDVSSFLMKDYM 120

Db 61 RVRRFDLKRILKMDRKAVETHLLRNPHVSDYRVLMAIGEDLDKSDVSSFLMKDYM 120

Qy 121 GRGKISKERSFLDVLEELKLNVAPDQDLERCLKLNTHRIDLTKTOKYKOSVQGAGT 180

Db 121 GRGKISKERSFLDVLEELKLNVAPDQDLERCLKLNTHRIDLTKTOKYKOSVQGAGT 180

Qy 181 SYRVLQAAIQKSLSKDPSSNFRM 203

Db 181 SYRVLQAAIQKSLSKDPSSNFRM 203

RESULT 10  
US-09-410-194-20  
Sequence 20, Application US/09410194

Patent No. US20020095030A1

GENERAL INFORMATION:

APPLICANT: Tschoopp, Jurg

APPLICANT: Thomé, Margot

APPLICANT: Burris, Kimberly

APPLICANT: Irmier, Marten

APPLICANT: Hahne, Michael

APPLICANT: Schrotter, Michael

APPLICANT: Schneider, Pascal

APPLICANT: Bodmer, Jean-Luc

APPLICANT: Steiner, Veronique

Rimoldi, Donata

APPLICANT: Hofmann, Kay

APPLICANT: French, E. Lars

TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS

FILE REFERENCE: 11141-002001

CURRENT APPLICATION NUMBER: US/09/410,194

CURRENT FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: PCT/EP98/01857

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2

PRIOR FILING DATE: 1997-04-01

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 20

LENGTH: 479

TYPE: PRT

ORGANISM: Homo sapiens

US-09-410-194-20

Query Match 16.6%; Score 410; DB 10; Length 479;

Best Local Similarity 26.1%; Pred. No. 1.9e-26;

Matches 137; Conservative 106; Mismatches 172; Indels 110; Gaps 22;

Qy 6 IHOVEALIDDEKEMLFLCRDVALDVPVPN---VRDLDDI---LREKGKLSVGDLA-- 56

Db 7 LYDIBGOLDSEDLASLKFLL---SIDYIPIORKQEPIKDAIMLFORQLERMLEPSNLSPL 62

Qy 57 -ELLYRVRFEDLILRKLMKDRAVETHLRLNP--HLYSDYRVLMAEIGEDLDKSDVSSII 113

Db 63 KELLFRINRDLDTYLNTREEMERE-LQTGPGRQISAYRMVLYQOISEVSSELRSRK 121

Qy 114 FLMKDYMGRGRISKEKLLVVEELKLNLVAPDOLDLILRKCLDNTHRLDKTOKYKQ 173

Db 122 FLLQEESRKCLDDDMNLDFIEMEKRTILGEKLDILRKVCQAQINKSLK1 INDYEE 180

Qy 174 -----SVOGAGTSYRNLYQAAIQKSLSKDPSPNNERLHNGRSKEQLRKGOLGAQEPYRK 226

Db 181 FSKERSSSLESPDETSNGEGLCG/TISPSRE----- 214

Qy 227 SIOSEAFALPOSIPERYKMKSKPGLICLIDCIG-----NETEL--- 266

Db 215 --QDSES-- OTL-DKVYQNSKPKPGYCILNNHNFAKAREKYPKHLSTDRNRGTHLDAG 268

Qy 267 -LRDFTTSLGTEVORFLHSMSHGTSQIQLGAFACAPHEHRIDTSFVCLVSRGGSOVYGD 325

Db 269 ALTTTFFEEELIFIEKPHDDCTVEQIYEILKTYQLM-DHSNNDCFCICCILSHGDGTIYGD 327

Qy 326 QTHSGSLPLHHTIRMFMDSCPYLAGKPKMFIO----NY---VVSEGOLENSESLEVD- 376

Db 328 GOEA--PIWEETSQPTGLKCPSLACKPKPFVQACQGDNFKQGPVETESEQYLEMM- 385

Db 377 -GPAMKKNFEKAQKRGCLCTVREADFWSLCTADMSSLLFOSHSSPSLYLQCLSQKLRO- 434

Qy 386 SSPOTRYIP-----DEFULLGMATVNCVSRRPAETWYIOSLCOSLRC 433

Qy 435 -RKRPLLDLHIELGWMYDINWSRVAKE- KIYWLQHQLRKL 476

Db 434 PRGDDLTILTEVN--YEVSNKDDKMKQMQPQTFLRKLY 475

RESULT 11  
US-09-864-761-35073  
Sequence 35073, Application US/09864761  
Parent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wenheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1  
SEQ ID NO: 35073  
LENGTH: 76  
TYPE: PT  
ORGANISM: Homo sapiens  
FEATURE:

Best Local Similarity 98.7%; Pred. No. 8.4e-26; Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 359 NYVSEGOLLENSSLEVDGAMKVEFKAAKQRGLCTVHREADFFWSLCTADMSLLEQSIS 418  
 Db 1 NYVSEGOLLEDSSESLLEVGDGAMKVEFKAAKQRGLCTVHREADFFWSLCTADMSLLEQSIS 60

Qy 419 SPSLYLQLCSQKLROE 434  
 Db 61 SPSLYLQLCSQKLROE 76

RESULT 12  
 US-09-952-768-4  
 ; Sequence 4, Application US/09952768  
 ; Patent No. US2002035242A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alnemri, Emad S.  
 ; Fernando-Alnemri, Teresa  
 ; Litwack, Gerald  
 ; Armstrong, Robert  
 ; Tomaselli, Kevin  
 ; TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE, NUCLEAR ACIDS ENCODING AND METHODS OF USE  
 ; NUMBER OF SEQUENCES: 75  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seed Intellectual Property Law Group  
 ; STREET: Suite 6300, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; ZIP: 98104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, version #1.30.  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/952,768  
 ; FILING DATE: 10-Sep-2001  
 ; CLASSIFICATION: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Christiansen, William T.  
 ; REGISTRATION NUMBER: 44,514  
 ; REFERENCE/DOCKET NUMBER: 480140.424C4  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 496 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-952-768-4

Query Match 15.4%; Score 381.5; DB 10; Length 496;  
 Best Local Similarity 24.7%; Pred. No. 5.1e-24;  
 Matches 136; Conservative 100; Mismatches 170; Indels 145; Gaps 21;

Qy 6 1HOYBEALDDDEKMLLFCLRDYADVVPPN---VRDLDDI--LRERGKLSVGDLA-- 56  
 Db 7 LYDGEQLESDLASLKF--SLDYIPQRKOEPIKDALMLFQRQEKRMLFNSLSPF 62

Query Match 15.4%; Score 381.5; DB 10; Length 496;  
 Best Local Similarity 24.7%; Pred. No. 5.1e-24;  
 Matches 136; Conservative 100; Mismatches 170; Indels 145; Gaps 21;

Qy 57 -ELLYRVRREFDLKLRLKMRKAVETHL--SLDYIPQRKOEPIKDALMLFQRQEKRMLFNSLSPF 62

Db 63 KELLFRINRDLITYLNRKEEMERELTPGRQASAYRFHFCRMSWAANSQCOTOSV 122

Qy 84 -LRNPHLYSDIVMLMABIGDLKSDVSSLFLMKGDKISKEKSFLDLVVELEK 140  
 Db 123 PFWRVDHL--IRVMLYQISEEVRSRSFKFLQEEISCKLDDDMNLDFIEMEK 180

Query Match 15.4%; Score 381.5; DB 10; Length 496;  
 Best Local Similarity 24.7%; Pred. No. 5.1e-24;  
 Matches 136; Conservative 100; Mismatches 170; Indels 145; Gaps 21;

Qy 141 LNLYAPDQLDLLEKLNKNIHRDLKTIQKYKOSVOGACTSYRNQIAOKSLKDPSNN 200  
 Db 181 RVLNGEGKDLIKRCAQINKSLKLI-INDYEFSKG----- 216

Qy 201 FRLHNGRSKEQLKEOLGAQQEPVKSIQSEAFPLPOSIPPEERYKMKSKPLGICLIDCI 260  
 Db 217 -----ELCGYMTMSDPREOSES--OTL-DKYQMKSKPRGYCLINHH 259

Qy 261 G-----NETEL---LRDTFTSLGAEVOKFLHLSMHGISOILQGACM 299  
 Db 260 NFAKAREKYPKLHSRDRNGTHLDAGALTTFEEHLFEIKPHMCTVGEIYEILKIQYLM 319

Qy 300 PEHRYDGSFVCVLYSRGGSSQVYGDOTHSGPLPLHIRMFMGDSPLCPYLAGPKMFIO- 358  
 Db 320 -DHSMADCFICLISHGDKGILYGTGDQEA-PIVELTSQFTGLKCPSSLAKPVFFQA 376

Qy 359 ---NY--VVSSEGOLENSSLLEYD--GPAMKVNVEFKAQKRGLCVHREADFFNSLCTAD 409  
 Db 377 CQGDYQKGIPVETDSEEQPYLENDSLSSPOTRYIP-----DEADFLIGMATVN 424

Qy 410 MSLLEOSHSSPSLTYLQCLSLQKROE-RKRPPLLDLHIELNGYMWDSNSVSAKE-KYYV 465  
 Db 425 NCVSYRNPAEGFTWYTQSLCSRERCPGDDILTVEVN--YEVSNKDKNMKGKOMP 481

Qy 466 WLQHTLRKLJ 476  
 Db 482 QPTFTLRKLV 492

RESULT 13  
 US-09-954-697-27  
 ; Sequence 27, Application US/09954697  
 ; Patent No. US20020106631A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alnemri, Emad S.  
 ; TITLE OF INVENTION: RECOMBINANT, ACTIVE CAPSASES AND USSES  
 ; TITLE OF INVENTION: RECOMBINANT, ACTIVE CAPSASES AND USSES  
 ; FILE REFERENCE: 480140.431D2  
 ; CURRENT APPLICATION NUMBER: US/09/954,697  
 ; CURRENT FILING DATE: 2001-09-14  
 ; NUMBER OF SEQ ID NOS: 116  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO: 27  
 ; LENGTH: 476  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 US-09-954-697-27

Query Match 15.0%; Score 370.5; DB 10; Length 476;  
 Best Local Similarity 24.1%; Pred. No. 4e-23;  
 Matches 133; Conservative 93; Mismatches 160; Indels 165; Gaps 20;

Qy 6 1HOYBEALDDDEKMLLFCLRDYADVVPPN---VRDLDDI--LRERGKLSVGDLA-- 56  
 Db 7 LYDGEQLESDLASLKF--SLDYIPQRKOEPIKDALMLFQRQEKRMLFNSLSPF 62

Qy 57 -ELLYRVRREFDLKLRLKMRKAVETHL--SLDYIPQRKOEPIKDALMLFQRQEKRMLFNSLSPF 62

Db 63 KELLFRINRDLITYLNRKEEMERELTPGRQASAYRFHFCRMSWAANSQCOTOSV 122

Qy 84 -LRNPHLYSDIVMLMABIGDLKSDVSSLFLMKGDKISKEKSFLDLVVELEK 140  
 Db 123 PFWRVDHL--IRVMLYQISEEVRSRSFKFLQEEISCKLDDDMNLDFIEMEK 180

Query Match 15.4%; Score 381.5; DB 10; Length 496;  
 Best Local Similarity 24.7%; Pred. No. 5.1e-24;  
 Matches 136; Conservative 100; Mismatches 170; Indels 145; Gaps 21;

Qy 141 LNLYAPDQLDLLEKLNKNIHRDLKTIQKYKOSVOGACTSYRNQIAOKSLKDPSNN 200  
 Db 181 RVLNGEGKDLIKRCAQINKSLKLI-INDYEFSKG----- 216

Qy 201 FRLHNGRSKEQLKEOLGAQQEPVKSIQSEAFPLPOSIPPEERYKMKSKPLGICLIDCI 260  
 Db 210 Y-----EFSKGEELCKV----- 239

Qy 261 G-----NETEL---LRDTFTSLGAEVOKFLHLSMHGISOILQGACM 299

RESULT 14  
US-09-962-834A-2  
; Sequence 2, Application US/09962834A  
; Patent No. US20020034813A1  
; GENERAL INFORMATION:  
; APPLICANT: Bowman, Michael  
; TITLE OF INVENTION: NOVEL PROTEASE  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 Cambridgepark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/962-834A  
; FILING DATE: 25-Sep-2001  
; CLASIFICATION: <Unknown>  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/675,123  
; FILING DATE: 1996-07-03  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; REFERENCE/DOCKET NUMBER: GI5276  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 521 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SOURCE/SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
; US-09-962-834A-2

Db 240 NFAKAREKVKPLHSTRDRNGTHDAGALTTFEELFEIKPHHDCTVEQIYELKIQLM 299  
Qy 300 PEHRDYDFIVCVLVRSGGQSOSVYGYDOTHSGPLHIRMFMGDSCPYLAKPKMFFIQ- 358  
Db 300 -DHSNNDCFICCLSLGKGLTIGDQEA--PIYELTSQFTGLKCPSSLAGKPKYFFQA 356  
Qy 359 ---NY---VVSEGOLENSSILEVD--GPAMKNEVFAQRGLCIVHREADEFWNSICTAAD 409  
Db 357 CGDNYQKQGIVETDSEQPYLEMDSLSSPTRYIP---DEADFLGMATVN 404  
Qy 410 MSLLEOSHSSPSLYLOCLSOKLROE--RKRPFLDLHIELNGMYDWNRSYSAKE--KYVV 465  
Db 405 NCVSYRNPAEGTWYIOSLCQSLRERCPRGDDILTLTEVN---YEVSNDKDKNNKGKOMP 461  
Qy 466 WLQHTLRKL 476  
Db 462 QPTFTLRKLV 472

Db 256 MQASANTLNSETSTPKRAAV-----YRMNRNRLCIVNNHSFTSLKDROCTHKDA 307  
Db 197 VTPPDKEAESYQGEELSVOTDVTKFLALPQESWQNKAQSGNBRATG-APSLVSRG 255  
Qy 216 QLGAAQEPVVKSIQEAFLPOSITPEERYKMKSKPLIGCILJ-----DCIG--NET 264  
Db 256 MQASANTLNSETSTPKRAAV-----YRMNRNRLCIVNNHSFTSLKDROCTHKDA 307  
Qy 265 ELLRDTFTSLGLEYQKFHLMSMGSQLQFACMPHEIRDYDFSCFVCLVSRGGSSVYGV 324  
Db 308 EILSHVQWLQGFTVHNHNTVKVEMVLOQKQKCNPAHADGDCFVFCLTHGRGAVYSS 367  
Qy 325 DQTHSGPLAHIRRPMGDSCPYLAKPKMFFIQNVVSB-QLENSSLLEVGDPMKVN 383  
Db 368 DE--ALIPIREIMSMHTALCPRLAEKPKLFIQ--ACQGEEIOPSVSIEADALNPEQA 422  
Qy 384 EFKAKOZRGLCTYHRADEFWSLCTADMSSLEQSHSSPSLYLQCL-SOKLRO--ERRKPLLD 441  
Db 423 PTSLOD---SIPAEDFLGLATPGYVSFRHEEGSWYTIOSLNLKKLVPRMLKFLE 478

RESULT 15  
US-09-410-194-21  
; Sequence 21, Application US/09410194  
; Patent No. US20020095030A1  
; GENERAL INFORMATION:  
; APPLICANT: Tschopp, Jurg  
; APPLICANT: Thome, Margot  
; APPLICANT: Burns, Kimberly  
; APPLICANT: Irmler, Marten  
; APPLICANT: Hahne, Michael  
; APPLICANT: Schrater, Michael  
; APPLICANT: Schneider, Pascal  
; APPLICANT: Bodmer, Jean-Luc  
; APPLICANT: Steiner, Veronique  
; APPLICANT: Rimoldi, Donata  
; APPLICANT: Hofmann, Ray  
; APPLICANT: French, E. Lars  
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS  
; FILE REFERENCE: 11141-002001  
; CURRENT APPLICATION NUMBER: US/09/410,194  
; CURRENT FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: PCT/EP98/01857  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2  
; PRIOR FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 27  
; SEQ ID NO: 21  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; LENGTH: 571  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-410-194-21

Query Match 13.1%; Score 323.5; DB 10; Length 521;  
Best Local Similarity 26.9%; Pred. No. 4.1e-19;  
Matches 131; Conservative 77; Mismatches 204; Indels 75; Gaps 19;

Qy 9 VEEALDTDEKMLFLCRDVAIDVVP-----PNVRDLDLILRERGKLSVGD--LAEL 58  
Db 27 IDSNLGVQDVENLKFCG---IGLYPNKLEKSSASDVEHLLAEDLSEEDPFIAEL 82  
Qy 59 LYRVRFFDLRKILKMDRAVETHLLRNPHLVDYSDVLLMAEIGEDLKDSDYSSLLFLMKT 118

Query Match 13.1%; Score 323.5; DB 10; Length 571;  
Best Local Similarity 26.9%; Pred. No. 4.6e-19;  
Matches 131; Conservative 77; Mismatches 204; Indels 75; Gaps 19;

Qy 9 VEEALDTDEKMLFLCRDVAIDVVP-----PNVRDLDLILRERGKLSVGD--LAEL 58  
Db 27 IDSNLGVQDVENLKFCG---IGLYPNKLEKSSASDVEHLLAEDLSEEDPFIAEL 82

Qy 59 LYVYRFDLKRILKMDRKAVETHLLRNPHLYSDYRVLMAEIGEDLDKSDYSSLIFLMKD 118  
 || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
 Db 83 LYIIRQKKLQH-LNCTKEVE-RLLPQRVSLFRNLVESEGIDSENLDADMFLKD 140  
 || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
 Qy 119 YMGRGKISKEKSFDLVVPELEKLNLVAPDQLLE-----KCLKNIHRDLKTKIQ- 169  
 || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
 Db 141 SLPK----TEMTSLSFLAFEROGKIDEDNLTCLEDLKCKTVPKLLNEKYKREKATOI 196  
 || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
 Qy 170 -----KVQSVIOG---AGTSYRNVLQAAQOKSLADP--SNNFRHLNGRSKEQBLKE 215  
 || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
 Db 197 VTPPVDKREAESTQGEELVSPDVKTFLEALQESWQNKHAGSSNGNRATNGAPSLSRG 255  
 || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
 Qy 216 OLGAQQEPVKKSIOQESEAFPLQSIPEERYKMKSKPLQTCLII-----DCIG--NET 264  
 || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
 Db 256 MOGASANTLNSETSTKRAV-----YRMARNHRLGLCVINNNHSTSLKDRQGTHKDA 307  
 || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
 Qy 265 ELLRDTFTSLGYEVQKFLHLSMHGISOQLGOFACMPERHDYDSFVCYVLVSRRGQSOSYGV 324  
 || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
 Db 308 EILSHVFWMLGFVHINNNVTKMEMAYLQOKCNPABADGDCFVFCLTHRGFAYYS 367  
 || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
 Qy 325 DOTHSGLPLHHIRRMFGDSCPYLAGPKMFQTONTVSEG-OLENSSLEYDGPAMKNV 383  
 || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
 Db 368 DE--ALIPTRTMSHTALQCPRLAEKPKLFFTQ---ACQGEETQPSVSIADALNPEQA 422  
 || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
 Qy 384 EFKAQKRGICTVIREADEFWSLCTADMSLQHSSPSLYLOCLSQKURQ--ERKRPLLD 441  
 || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
 Db 423 PTSQD---SIPAEDFLGLGLATVPGYVSFRHVEEGSWYIQLSCNHLKLYPRMLKFLE 478  
 || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
 Qy 442 LHIELNG 448  
 || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
 Db 479 KTMEIRG 485

Search completed: April 12, 2003, 22:40:49  
 Job time : 22.2268 secs

GenCore version 5.1.4\_P5\_4578  
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## OM protein - protein search, using sw model

Run on: April 12, 2003, 20:50:13 ; Search time 19.8573 Seconds  
(without alignments)  
711.223 Million cell updates/sec

Title: US-09-380-546A-2  
Perfect score: 2473  
Sequence: 1 MSAEVTHQVEEALDTDEKEM. .... EKYYVWLOHTLRKKLILSYT 480

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext. 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:  
1: /cgns2\_6/podata/1/1aa/5A\_COMB.pep:  
2: /cgns2\_6/podata/1/1aa/5B\_COMB.pep:  
3: /cgns2\_6/podata/1/1aa/6A\_COMB.pep:  
4: /cgns2\_6/podata/1/1aa/6B\_COMB.pep:  
5: /cgns2\_6/podata/1/1aa/PCTUS\_COMB.pep:  
6: /cgns2\_6/podata/1/1aa/backfiles1.pep:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2468	99.8	480	4 US-09-795-088A-2	Sequence 2, Appli
2	2412	97.5	480	4 US-09-069-023-34	Sequence 34, Appli
3	2265.5	91.6	445	3 US-08-859-167-2	Sequence 2, Appli
4	2265.5	91.6	445	3 US-09-109-173-2	Sequence 2, Appli
5	2265.5	91.6	445	4 US-09-226-993-2	Sequence 2, Appli
6	1007	40.7	221	4 US-09-382-155-17	Sequence 17, Appli
7	1007	40.7	221	4 US-09-074-04A-17	Sequence 17, Appli
8	417	16.9	84	4 US-09-074-04A-2	Sequence 2, Appli
9	410	16.6	479	4 US-08-983-502-7	Sequence 7, Appli
10	410	16.6	479	5 PCT-US96-10521-7	Sequence 7, Appli
11	408	16.5	479	4 US-08-807-200-12	Sequence 12, Appli
12	408	16.5	479	4 US-09-382-155-28	Sequence 12, Appli
13	406	16.4	479	3 US-08-852-782-3	Sequence 3, Appli
14	404.5	16.4	464	4 US-08-983-502-18	Sequence 18, Appli
15	404.5	16.4	464	5 PCT-US96-10521-18	Sequence 2, Appli
16	403	16.3	84	4 US-09-882-155-2	Sequence 28, Appli
17	403	16.3	479	4 US-09-382-155-28	Sequence 27, Appli
18	403	16.3	479	4 US-09-001-777-12	Sequence 28, Appli
19	403	16.3	479	4 US-09-074-04A-28	Sequence 26, Appli
20	400	16.2	479	4 US-09-074-04A-26	Sequence 26, Appli
21	397	16.1	479	4 US-09-382-155-27	Sequence 27, Appli
22	392	15.9	479	4 US-09-382-155-26	Sequence 26, Appli
23	384	15.5	78	4 US-09-382-155-1	Sequence 1, Appli
24	384	15.5	78	4 US-09-074-04A-27	Sequence 1, Appli
25	381.5	15.4	496	4 US-08-665-220-4	Sequence 4, Appli
26	381.5	15.4	496	4 US-09-291-692-4	Sequence 4, Appli
27	370.5	15.0	476	4 US-09-561-756-27	Sequence 27, Appli

ALIGNMENTS					
RESULT 1					
US-09-795-088A-2	Sequence 2, Application US/08795088A	Patent No. 6245569	GENERAL INFORMATION:		
			APPLICANT: Sul, Hong-Bing		
			APPLICANT Goeddel, David V.		
			TITLE OF INVENTION: Regulators of Apoptosis		
			NUMBER OF SEQUENCES: 3		
			CORRESPONDENCE ADDRESS:		
			ADDRESSSEE: Science & Technology Law Group		
			STREET: 75 Denise Drive		
			CITY: Hillsborough		
			STATE: California		
			COUNTRY: USA		
			ZIP: 94010		
			COMPUTER READABLE FORM:		
			MEDIUM TYPE: Floppy disk		
			COMPUTER: IBM PC compatible		
			OPERATING SYSTEM: PC-DOS/MS-DOS		
			SOFTWARE: PatentIn Release #1.0, Version #1.30		
			CURRENT APPLICATION DATA:		
			APPLICATION NUMBER: US/08/795, 088A		
			FILING DATE:		
			CLASSIFICATION: 435		
			ATTORNEY/AGENT INFORMATION:		
			NAME: Osman, Richard A.		
			REGISTRATION/DOCKET NUMBER: T97-001		
			TELECOMMUNICATION INFORMATION:		
			TELEPHONE: (650) 343-4341		
			TELEFAX: (650) 343-4342		
			INFORMATION FOR SEQ ID NO: 2:		
			SEQUENCE CHARACTERISTICS:		
			LENGTH: 480 amino acids		
			TYPE: amino acid		
			STRANDEDNESS: not relevant		
			TOPOLOGY: not relevant		
			MOLECULE TYPE: Peptide		
			US-08-795-088A-2		
			Query Match Similarity 99.8%; Pred. No. 1e-230; Indels 0; Gaps 0;		
			Matches 479; Conservative 1; Mismatches 0;		
Qy	1 MSAEVTHQVEEALDTDEKEM. .... EKYYVWLOHTLRKKLILSYT	60			
Db	1 MSAEVTHQVEEALDTDEKEM. .... EKYYVWLOHTLRKKLILSYT	60			
Qy	61 RVRRPFDLLKRILKMDRKAVETHLLRNPHLVSDYRVLMAIEGDLDKSDYSSLLFLMDYM	120			

RESULT 2  
 / Sequence 09-023-34 Application US/09069023A  
 ; Patent No. 6348573  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nunez, Gabriel  
 ; APPLICANT: Inohara, Naohiro  
 ; APPLICANT: Koseki, Takeyoshi  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
 ; FILE REFERENCE: UM-03333  
 ; CURRENT FILING DATE: 1998-04-27  
 ; NUMBER OF SEQ ID NOS: 38  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO: 34  
 ; LENGTH: 480  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-069-023-34

*not in claim*

Query Match 97 %; Score 2412; DB 4; Length 480;  
 Best Local Similarity 97 %; Pred. No. 2.7e-225;  
 Matches 469; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

1 MSAEVTHOEEALDDEKMLEFLCRDVAYDVPNVRLDILRERGKLSVGDLAELLY 60  
 1 MSAEVTHOEEALDDEKMLEFLCRDVAYDVPNVRLDILRERGKLSVGDLAELLY 60

Qy 61 RVRFDLKRILKMDRKAVETHLNRPHYSYDVRMLKDYM 120  
 Db 61 RVRFDLKRILKMDRKAVETHLNRPHYSYDVRMLKDYM 120

Qy 121 GRGKISKEKSFLDLYVELEXLNLYAPDQDLLEKLNTHRIDLTKTKIOKYKOSVOGACT 180  
 Db 121 GRGKISKEKSFLDLYVELEXLNLYAPDQDLLEKLNTHRIDLTKTKIOKYKOSVOGACT 180

Db 121 GRGKISKEKSFLDLYVELEXLNLYAPDQDLLEKLNTHRIDLTKTKIOKYKOSVOGACT 180

Qy 181 SYRNVLQAIQSLKDPSNFRLINGRSKEORLKEQLGAAQEPVKKS10SEQEAFLP0S1P 240  
 Db 181 SYRNVLQAIQSLKDPSNFRLINGRSKEORLKEQLGAAQEPVKKS10SEQEAFLP0S1P 240

Qy 241 EERYKMKSKPLGICLIDCIGNETLRLDFTSLGYEVQFLHLSMHS1SQILQFACMP 300  
 Db 241 EERYKMKSKPLGICLIDCIGNETLRLDFTSLGYEVQFLHLSMHS1SQILQFACMP 300

RESULT 3  
 / Sequence 2 Application US/08859167  
 ; Patent No. 6037461  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alnemri, Emad S.  
 ; APPLICANT: Fernandez-Alnemri, Teresa  
 ; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF  
 ; TREATMENT USING THE SAME, AND COMPOSITIONS FOR AND METHODS  
 ; OF MAKING THE SAME  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & NO. 6037461r1s  
 ; STREET: One Liberty Place,  
 ; CITY: Philadelphia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: WINDOWS  
 SOFTWARE: WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/859,167  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DeLuca, Mark  
 REGISTRATION NUMBER: 33,229  
 REFERENCE/DOCKET NUMBER: T-JU-  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-3100  
 TELEFAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 445 amino acids  
 TYPE: Linear  
 MOLECULE TYPE: protein  
 US-08-859-167-2

Query Match 91.6%; Score 2265.5; DB 3; Length 445;  
 Best Local Similarity 92.5%; Pred. No. 3.8e-211;  
 Matches 444; Conservative 1; Mismatches 0; Indels 35; Gaps 1;

Qy 1 MSAEVTHOEEALDDEKMLEFLCRDVAYDVPNVRLDILRERGKLSVGDLAELLY 60  
 Db 1 MSAEVTHOEEALDDEKMLEFLCRDVAYDVPNVRLDILRERGKLSVGDLAELLY 60

Qy 61 RVRFDLKRILKMDRKAVETHLNRPHYSYDVRMLKDYM 120  
 Db 61 RVRFDLKRILKMDRKAVETHLNRPHYSYDVRMLKDYM 120

Qy 121 GRGKISKEKSFLDLYVELEXLNLYAPDQDLLEKLNTHRIDLTKTKIOKYKOSVOGACT 180  
 Db 121 GRGKISKEKSFLDLYVELEXLNLYAPDQDLLEKLNTHRIDLTKTKIOKYKOSVOGACT 180

Qy 181 SYRNVLQAIQSLKDPSNFRLINGRSKEORLKEQLGAAQEPVKKS10SEQEAFLP0S1P 240  
 Db 181 SYRNVLQAIQSLKDPSNFRLINGRSKEORLKEQLGAAQEPVKKS10SEQEAFLP0S1P 240

Qy 241 EERYKMKSKPLGICLIDCIGNETLRLDFTSLGYEVQFLHLSMHS1SQILQFACMP 300  
 Db 241 EERYKMKSKPLGICLIDCIGNETLRLDFTSLGYEVQFLHLSMHS1SQILQFACMP 300

Qy 181 SYRNVLQAIQSLKDPSNFRHLNGRSKEORLKEQLGAAQEPVKKS10SEQEAFLP0S1P 240  
 Db 181 SYRNVLQAIQSLKDPSNFRHLNGRSKEORLKEQLGAAQEPVKKS10SEQEAFLP0S1P 240

RESULT 4  
US-09-109-273-2  
Sequence 2, Application US/09109273  
Patent No. 6063760

GENERAL INFORMATION:  
 APPLICANT: Alnemri, Emaad S.  
 ATTORNEY/AGENT: Fernandez-Alnemri, Teresa  
 TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF  
 TREATING CANCER AND COMPOSITIONS FOR AND METHODS  
 OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS  
 OF MAKING THE SAME  
 NUMBER OF SEQUENCES: 17

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & NO. 6063760r1s  
 STREET: One Liberty Place, 46th floor  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: WINDOWS  
 SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/109,273  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/859,167  
 FILING DATE: 08/27/1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DeLuca, Mark  
 REGISTRATION NUMBER: 33-229  
 REFERENCE/DOCKET NUMBER: TJU-TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-3100  
 TELEFAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 445 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-09-109-273-2

Query Match 91.6%; Score 225.5; DB 3; Length 445;  
 Best Local Similarity 92.5%; Pred. No. 3.8e-211;  
 Matches 444; Conservative 1; MisMatches 0; Indels 35; Gaps 1;

Qy 1 MSAEVTHQEELPDTEKEMLFLCRDVAIDVPPNVRDLDDLRERGKLSYGDLLAEYL 60  
 Db 1 RVRRFDLKRILKMDRKAVETHLLRNPHVSRYVLMAEIGEDLDKSDVSSLIFLMKDYM 120

Db 61 RVRRFDLKRILKMDRKAVETHLLRNPHVSRYVLMAEIGEDLDKSDVSSLIFLMKDYM 120

Qy 121 GRSKISKERSFLDLYVELEKLNLVAPDOLDEKCNKLNHIDLTKTIOKYKOSVOQAGT 180  
 Db 121 GRSKISKERSFLDLYVELEKLNLVAPDOLDEKCNKLNHIDLTKTIOKYKOSVOQAGT 180

Qy 181 SYRNVLQAIQSKLDPENNFRLHNGRSKEQRQLKEQLGAAQQEPVKSTOESEAFLPOSIP 240  
 Db 181 SYRNVLQAIQSKLDPNNFR-----SIP 205

Qy 241 EERYKMSKPLGLCILIDCIGNETELLRDTFTSLGYEVOKFLHLSMHISQ1LGQFACMP 300  
 Db 206 EERYKMSKPLGLCILIDCIGNETELLRDTFTSLGYEVOKFLHLSMHISQ1LGQFACMP 265

Qy 301 EHDDYDSFVCVLYSRGGSSVYGVQDTHSGLPDUHTRMFMGDSCPYLAKPKMFHQNY 360  
 Db 266 EHDDYDSFVCVLYSRGGSSVYGVQDTHSGLPDUHTRMFMGDSCPYLAKPKMFHQNY 325

Qy 361 VYSEGOLENSSLLEVDPAMKNEFEKAQKRGCLCTVHREADFWSLCTADMSSLEQSHSSP 420  
 Db 326 VYSEGOLENSSLLEVDPAMKNEFEKAQKRGCLCTVHREADFWSLCTADMSSLEQSHSSP 385

Qy 421 SLYLQLCISOKLQRERKRPFLDHLIELNCYMDWNSRVSAKEKYYVWLOHTLRKKLILSYT 480  
 Db 386 SLYLQLCISOKLQRERKRPFLDHLIELNCYMDWNSRVSAKEKYYVWLOHTLRKKLILSYT 445

RESULT 5  
US-09-276-993-2  
Sequence 2, Application US/09276993  
 ; Patent No. 6207601  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fernandez-Alnemri, Teresa  
 ; ATTORNEY/AGENT: Alnemri, Emaad S.  
 ; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF  
 ; TREATING CANCER AND COMPOSITIONS FOR AND METHODS  
 ; OF MAKING THE SAME  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & NO. 6207601r1s  
 ; STREET: One Liberty Place, 46th floor  
 ; CITY: Philadelphia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; COMPUTER: IBM PC compatible  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: WINDOWS  
 ; SOFTWARE: Wordperfect  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/276,993  
 ; CLASSIFICATION:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/859,167  
 ; FILING DATE: 08/27/1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: DeLuca, Mark  
 ; REGISTRATION NUMBER: 33-229  
 ; REFERENCE/DOCKET NUMBER: TJU-TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 568-3100  
 ; TELEFAX: (215) 568-3439  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 445 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein

US-09-276-993-2

Query Match 91.6%; Score 225.5; DB 3; Length 445;  
 Best Local Similarity 92.5%; Pred. No. 3.8e-211;  
 Matches 444; Conservative 1; MisMatches 0; Indels 35; Gaps 1;

Qy 1 MSAEVTHQEELPDTEKEMLFLCRDVAIDVPPNVRDLDDLRERGKLSYGDLLAEYL 60  
 Db 1 RVRRFDLKRILKMDRKAVETHLLRNPHVSRYVLMAEIGEDLDKSDVSSLIFLMKDYM 120

Qy 61 RVRRFDLKRILKMDRKAVETHLLRNPHVSRYVLMAEIGEDLDKSDVSSLIFLMKDYM 120

Query Match 91.6%; Score 2265.5; DB 4; Length 445;  
 Best Local Similarity 92.5%; Pred. No. 3.8e-211; Mismatches 1; Indels 35; Gaps 1;  
 Matches 444; Conservative 1; Gaps 0;

Oy 1 MSAEVHQVEEALDTDEKEMILFLCRDVAIDVPPNVRDLDLILRERGKLSVGDLAELLY 60  
 Db 1 MSAEVHQVEEALDTDEKEMILFLCRDVAIDVPPNVRDLDLILRERGKLSVGDLAELLY 60

Qy 61 RVRFDLIKRILKMDRKAVETHLLRNPHVSVDYRVLMAIGEDLDKSDSSLIPLMKDM 120  
 Db 61 RVRFDLIKRILKMDRKAVETHLLRNPHVSVDYRVLMAIGEDLDKSDSSLIPLMKDM 120

Qy 121 GRGISKEKSFELDVVELEKLNLVAPDQLLEKLNKNIHRIDLTKTQKVKOSVQGAGT 180  
 Db 121 GRGISKEKSFELDVVELEKLNLVAPDQLLEKLNKNIHRIDLTKTQKVKOSVQGAGT 180

Qy 121 GRGISKEKSFELDVVELEKLNLVAPDQLLEKLNKNIHRIDLTKTQKVKOSVQGAGT 180  
 Db 121 GRGISKEKSFELDVVELEKLNLVAPDQLLEKLNKNIHRIDLTKTQKVKOSVQGAGT 180

Qy 181 SYRNLQAIIQKSLKDPNSNFR 203  
 Db 181 SYRNLQAIIQKSLKDPNSNFR 203

RESULT 7 US-09-074-044A-17  
 Sequence 17; Application US/09074044A  
 GENERAL INFORMATION:  
 Patent No. 6207458  
 APPLICANT: CHAUDHARY, PREET M  
 ADDRESS: HOOD, LEROY  
 TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND  
 NUMBER OF SEQUENCES: 28  
 CORRESPONDENCE ADDRESS:  
 STREET: 2405 GRAND BLVD., SUITE 400  
 CITY: KANSAS CITY  
 STATE: MISSOURI  
 COUNTRY: USA  
 ZIP: 64108  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/074,044A  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: COLLINS, JOHN M  
 REGISTRATION NUMBER: 26,262  
 TELECOMMUNICATION INFORMATION:  
 REFERENCE/DOCKET NUMBER: 26588  
 TELEPHONE: 816/474-9050  
 TELEFAX: 816/474-9057  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 221 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE: Homo sapiens  
 US-09-074-044A-17

Query Match 40.7%; Score 1007; DB 4; Length 221;  
 Best Local Similarity 99.5%; Pred. No. 1.2e-89; Mismatches 0; Indels 0; Gaps 0;  
 Matches 202; Conservative 1; Gaps 0;

Qy 1 MSAEVHQVEEALDTDEKEMILFLCRDVAIDVPPNVRDLDLILRERGKLSVGDLAELLY 60  
 Db 1 MSAEVHQVEEALDTDEKEMILFLCRDVAIDVPPNVRDLDLILRERGKLSVGDLAELLY 60

Qy 61 RVRFDLIKRILKMDRKAVETHLLRNPHVSVDYRVLMAIGEDLDKSDSSLIPLMKDM 120  
 Db 61 RVRFDLIKRILKMDRKAVETHLLRNPHVSVDYRVLMAIGEDLDKSDSSLIPLMKDM 120

Qy 121 GRGISKEKSFELDVVELEKLNLVAPDQLLEKLNKNIHRIDLTKTQKVKOSVQGAGT 180  
 Db 121 GRGISKEKSFELDVVELEKLNLVAPDQLLEKLNKNIHRIDLTKTQKVKOSVQGAGT 180

Qy 181 SYRNLQAIIQKSLKDPNSNFR 203  
 Db 181 SYRNLQAIIQKSLKDPNSNFR 203

RESULT 8

US-09-044A-2  
Sequence 2, Application US/09074044A  
; Patent No. 6207458

GENERAL INFORMATION:  
APPLICANT: CHAUDHARY, PREET M  
APPLICANT: HOOD, LEROY  
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NK-KB, JNK AND  
TITLE OF INVENTION: APOPTOSIS PATHWAYS AND METHODS OF USING THE SAME  
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOODY, WILLIAMS, TIMMONS & COLLINS  
STREET: 2405 GRAND BLVD., SUITE 400  
CITY: KANSAS CITY  
STATE: MISSOURI  
COUNTRY: USA  
ZIP: 64108

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/074, 044A  
FILING DATE: 16-JAN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: COLLINS, JOHN M  
REGISTRATION NUMBER: 26,762  
REFERENCE/DOCKET NUMBER: 26588

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 816/474-9050  
TELEFAX: 816/474-9057

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 84 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: not relevant

MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens

US-09-074-044A-2

Query Match 16.9%; Score 417; DB 4; Length 84;  
Best Local Similarity 100.0%; Pred. No. 4.2e-33; Gaps 0;  
Matches 84; Conservative 0; Mis matches 0; Indels 0; Gaps 0;

Qy 90 VSDYRVLMPKEIGEDLKSVDSSLJFLMKDYMGRGKISKEKSFLDVYVELEKLNIVADPQL 149  
Db 1 VSDYRVLMPKEIGEDLKSVDSSLJFLMKDYMGRGKISKEKSFLDVYVELEKLNIVADPQL 60

Qy 150 DLLEKCLAKNIHRIDLTKTQKYKO 173  
Db 61 DLLEKCLAKNIHRIDLTKTQKYKO 84

RESULT 9  
US-09-98-502-7  
Sequence 2, Application US/08983502  
; Patent No. 6399327

GENERAL INFORMATION:  
APPLICANT: David WALLACH  
APPLICANT: Mark P. BOLDIN  
APPLICANT: Tanya M. GONCHAROV  
APPLICANT: Yury V. GOLSEEV

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS  
TITLE OF INVENTION: AND OTHER PROTEINS  
NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brody and Neimark  
STREET: 419 Seventh Street N.W., Ste. 300  
CITY: Washington

STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/983, 502  
FILING DATE: 16-JAN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10521  
FILING DATE: 14-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 114, 615  
FILING DATE: 16-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 114, 986  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 115, 319  
FILING DATE: 14-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 116, 588  
FILING DATE: 27-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 117, 932  
FILING DATE: 16-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Brody, Roger L.  
REGISTRATION NUMBER: 25, 618  
REFERENCE/DOCKET NUMBER: WALLACH-19  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 479 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-983-502-7

Query Match 16.6%; Score 410; DB 4; Length 479;  
Best Local Similarity 26.1%; Pred. No. 3.1e-31;  
Matches 137; Conservative 106; Mismatches 172; Indels 110; Gaps 22;

Qy 6 IHOVEALDTDEKEMLLPFLCRDVAIDVPPN---VRDLDI---LRERGKLSVGDLA-- 56  
Db 7 LYDGEQDLEDSLASKFL---SLDYIPQRKQEPIDALMELQRQEPKRMLESNSFPL 62

Qy 57 -ELLYYVRVRFDLKRLKMDRKAVETHILLRNP-HLYSDYRVLMAEIGEDLKDSDVSSLI 113  
Db 63 KELLFRINRDLILTYLTNRKEEMRE-LQTPCRQDSAYRMLQYSEEVRSERSLSRFK 121

Qy 114 FLKDMYMRGKTSKEKSFLDVYVELEKLNIVADPQLLELKLNIVADLTKTQKYKO 173  
Db 122 FLLQEIESKCKLDDMNLDFIEMERVILGEKGKDLIKRYCAQINKSLKI-INDYE 180

Qy 174 ----SVQAGACTSYRNVLQIAIOKSLSKDPSPNFRLHNGRSKEQLIKEQLGAQQEPVK 226  
Db 181 FSKERSSSLEGSDDEFSGEELGVMITSDPRE----- 214

Qy 227 S1QESDAFLPOSTPEERYKMKSKPLGICLITDCIG-----NETEL--- 266  
Db 215 --OPSES--OTU-DKYQMKSKPGRQYCLINHHNFKAAREVPKHLISIRDNGTHIDAG 268

Qy 267 -LRDFTFSLGLEYQFKLHSMGISQIQGPACMPHDYDSFVCVLVSRSQGSOSVQVGD 325  
Db 269 ALTTTFEEFLHFETKPHDDCTVEQIYETLKVQLM-DHSNMDCFCITLSSHGDKGKJYGTG 327



SEQUENCE CHARACTERISTICS:  
; LENGTH: 479 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: Internal  
; US-09-001-777-12

Query Match 16.5%; Score 408; DB 4; Length 479;  
; Best Local Similarity 26.1%; Pred. No. 4.8e-31;  
; Matches 137; Conservative 105; Mismatches 173; Indels 110; Gaps 22;

Qy 6 IHOVEEALDTDEKEMLIFLPCRDYVDPVN---VRDLDI---LRERGKLSVGDLA-- 56  
; Db 7 LYDIEQOLDSEDLASLKF---SLDYIPQRKOEPIKDALMFLQRQEKRMLESNLNSFL 62

Qy 57 -ELLYRVRFDLKLKRILKMDRKAVETHLLRNP---HLYSDYRVLMAEGDLOKSDVSSLI 113  
; Db 63 KELLFRINRDLITYLNTKEEMER-LQTGRQAISAYRMLQISESEVSSELRSFK 121

Qy 114 FLMKDYMGRGKISKEKSPLDVLVYAPQDLDLEKCLKNIHRIDLTKKIQVKQ 173  
; Db 122 FLLQEEISCKLDDMNLLDIFTEMERKRYTIGSKLDLKRYTAQINSLLKI-INDYE 180

Qy 174 -----SVOGAGTSYRNVLQAAQOKPSNNFRLHNGRSKEQLKEQGAQQEPYKK 226  
; Db 181 FSKERSSSLEGSPDEFNSEELCGVMTISDSPRE-----

Qy 227 SIOSEAFAPPOSTPQKPLGICLIDCIG-----NETEL--- 266  
; Db 215 -QDSES---QTL-DKVQOMKSKRPGYCILINHNFAKAREKVPKLHSIRDNGTHLDAG 268

Qy 267 -LRDFTTSIIGYEYOKFLHLMSMHGTSQTLQGQFACMPHRDYDSTPVCVLVRGGQSQSYGV 325  
; Db 269 ALTTFFEEHFEKPKHDDOTPEQIYEILKLYIQLM-DHSMNDCTFCICCILSHGDGIFTYGD 327

Qy 326 QTHSGLPLAHIRFMGDSCPYLAKPKMFQI---NY---VVSESQLENSSLLVEY- 376  
; Db 328 GOEP--PIVELTSQFTGLKPCPLASLGPKWIFIQACQDGNYQRTPVEDSEEQPYLENDL 385

Qy 377 -GPANKRNVEKAQFRGLCTVHREADFFWNLCTQSCQKLROE- 434  
; Db 386 SSQTRYIP-----DEADFLGGMATNNCYSRNPAEGTWYIQSLCQSLRERC 433

Qy. 435 -RKRLLDLHTELINGMYDWNRSYSAK--KYYWLQHTLRKLLI 476  
; Db 434 PRGDILTILTEVN---TEVSNRDKKNGKQMPQPTFLRKLV 475

RESULT 12  
; US-09-001-777-12  
; Sequence 12, Application US/09001777  
; GENERAL INFORMATION:  
; Patent No. 6172130  
; APPLICANT: Hunter, John J.  
; APPLICANT: Shyjan, Andrew W.  
; APPLICANT: Wong, Grace H.W.  
; TITLE OF INVENTION: NOVEL FORMS OF CASPASE-8 AND USES THEREOF  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/001,777  
; FILING DATE: 31-DEC-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/807,200  
; FILING DATE: 27-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Freeman, John W.  
; REGISTRATION NUMBER: 29,066  
; REFERENCE/DOCKET NUMBER: 07334/021002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEX: 617/542-8906  
; TELEFAX: 200154  
; INFORMATION FOR SEQ ID NO: 12:

RESULT 13  
; US-08-852-782-3  
; Sequence 3, Application US/08852782  
; Patent No. 608042  
; GENERAL INFORMATION:  
; APPLICANT: Vishva Dixit, Kristine Kikly, Jian Ni, Craig Rosen and Steven Ruben  
; TITLE OF INVENTION: INTERLEUKIN-1 BETA CONVERTING ENZYME LIKE APOPTOTIC PR  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-2799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/852,782  
; FILING DATE:

CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
     APPLICATION NUMBER: 60/019,365  
     FILING DATE: 05 JUNE 1996  
     APPLICATION NUMBER: 60/017,454  
     FILING DATE: 17 MAY 1996  
     APPLICATION NUMBER: 60/017,914  
     FILING DATE: 16 MAY 1996  
 ATTORNEY/AGENT INFORMATION:  
     NAME: Han, William T  
     REGISTRATION NUMBER: 34,344  
     REFERENCE/DOCKET NUMBER: P50484-2  
 TELECOMMUNICATION INFORMATION:  
     TELEPHONE: 610-270-5219  
     TELEFAX: 610-270-5090  
     TELEX:  
         INFORMATION FOR SEQ ID NO: 3:  
         SEQUENCE CHARACTERISTICS:  
         LENGTH: 479 amino acids  
         TYPE: amino acid  
         STRANDEDNESS: single  
         TOPOLOGY: linear  
         MOLECULE TYPE: Peptide  
         HYPOTHETICAL: NO  
         ANTI-SENSE: NO  
         FRAGMENT TYPE: N-terminal  
         ORIGINAL SOURCE:  
         -08-852-782-3

Query Match      16.4%;      Score 406;      DB 3;      Length 479;  
 Best Local Similarity 26.4%;      Pred. No. 7.5e-31;  
 Matches 137;      Conservative 105;      Mismatches 173;      Indexes 110;      Gaps 22;

6	IHQYEBALDPDEKEMLFGLRDVAIDVPPNN---VRDLIDI--LREGRKLGVGDLLA--	56
7	SIDYIIPQRKQEPFKDAMLFQRIQKRMELFEESSLUSF	62
57	-ELLYRVRPFDLKLTKMRDKAVETHLLRNP--HLVSDYRVLMAIGEFLDLDKSDVSSL	113
63	KELLPRINRDLILTYLNTKEEMERE-LQPGRQIAISAVRLMTOISEYTSRSERSFSK	121
114	FLMKYGMGRKISKESKFELDYLVELEKLNLYAPDQLDLFLKCLKNITHRDLTKTOKYKO	173
122	FLLQEIBSKQLDDDNLDFIEMKRVTLGEKGKDILKRVCAOJNKSLSIKI-INDYE	180
174	---SVQGAGTSTKRNVLQIAQIKSLKDPSSNNFLHNGRSKEQLKEQLGAAQOEPVK	226
181	FSKERSSSLLESPDSEPSGEEPLCGVNTISDSPRE-----	214
227	SIQESEAFLPPOSITPERYKNSKPKLIGICLIIIDCIG-----NETEL--	266
215	-QDSES--QTL-DKVIQMSKSPRGYCLINNNHNFPAKAREKVPKLNHSIRDRNGTHLDAG	268
267	-LRDFTTSIAGYEVOKEFLHLSMHGITSQILOFACMPCEHRDYDSFVCVLYSGGSOSYYGV	325
269	ALTTRTEELHEIKPHIDDCTEQIYELLKTYQLM-DHSNMDCFICCLSHGDKGIIYGTID	327
326	QTHSGSPLLHJRRRMFGDCSPYPLAGAKPMFFIQ----NY--VVSEBQLENSSLLEV	376
328	GQEP--PIYETTSQFGLKCSLAGRKFVFFQACQDNYXQKGPVETDSSEQPYLMDL	385
377	-GPAMKNEVFKAQKRGJLCTYHREADFEWSLCTADMSELQSHSSPSLYLOCISQKLROE-	434
386	SSPQTWIP-----DEADFLGMLTAGVNVCYSYRPAEGTYQISLWQSRLRERC	433
435	-RKRPDLDLHJELNGYMWDWSRSVSAKE-KYVWLOHTLRRKLI	476
434	PRGDDILITLIEVN--YEVSNIKKDDKRNMGROMQPPTFTLRLKKV	475

RESULT 14  
-08-98-502-18

Sequence 18, Application US/089833502

QY 174 SVQAGTSYRNVLQAAIQKSLKDPSNNFLHNGRSKEORLKEQLGAQQEPVYKKSIQSEA 233  
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 181 FSKG -----NETEL---LRDTFT 272  
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 QY 234 FLFQSPTEERYKMKSKPGICLJIDCG-----NETEL---LRDTFT 272  
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 205 ---QTL DKVYQMKSKPGICLJIDCG-----NETEL---LRDTFT 272  
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 QY 273 SLGYEVOKFLHLMSMGSQLQFACMPHEHDYDFCVLYSRRGGSSOSVYCYDOTHSGLP 332  
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 261 EHFIEPKHDCTEDEQYEILKIQYL-DHSIMDCFCICCILSHDGKGIYCTDQPA--P 317  
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 QY 333 LHHRIRMFMDSCPYLAGKPMFFIQ----NY--VVSEQLENSSLVEYD--GPAMKN 382  
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 318 IYELTSQFTGLKPCPSLAGKPKVFFIQACQGDNYQKGIPVENDSEQYLENDLSSQTRY 377  
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 383 VEEKAQKRGGLCTVHREADFFWNSLCATADMSLLEQSHSSPSLYLQCLSQKLROE--RKRPLL 440  
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 378 IP-----DEADFLGGMATVNCYSYRNPAEGTWYIQSICOSLRLRCPRGDDIL 425  
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 441 DLHIELNGMYDWNRSYAKE-KYYWLQHTLRLKKLI 476  
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 426 TILTEVN--YEVSNKDDKKNNGKQMPQPTFLRLKKLV 460  
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 15

PCT-US96-10521-18

; Sequence 18, Application PC/TUS9610521

; GENERAL INFORMATION:

; APPLICANT: MODULATORS OF THE FUNCTION OF FAS RECEPTORS

; TITLE OF INVENTION: AND OTHER PROTEINS

; NUMBER OF SEQUENCES: 34

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/10521

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 114, 615

FILING DATE: 16-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 114, 986

FILING DATE: 17-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 115 , 319

FILING DATE: 14-SEP-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 116 , 588

FILING DATE: 27-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 117 , 932

FILING DATE: 16-APR-1996

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 464 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US96-10521-18

Query Match 16.4%; Score 404.5; DB 5; Length 464;  
 Best Local Similarity 26.3%; Pred. No. 1e-30;  
 Matches 136; Conservative 101; Mismatches 170; Indels 111; Gaps 56

6 IHQVEEALTDDBREMLFLCRDVAIDVPPN---VRDLDDI---LRERGKLSSGDLA--

GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2003, 20:46:38 ; Search time 137.706 Seconds

(without alignments)  
14287.562 Million cell updates/sec

Title: US-09-380-546a-1  
Perfect score: 2243

Sequence: 1 ggacgtcgaggcattacaat.....ctctttaaaaaaaaaa 2243  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_NA:\*

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1: /cgn_6/ptodata/2/pubpna/us07_pubcomb.seq:*
2: /cgn2_6/ptodata/2/pubpna/pct_new_pub.seq:*
3: /cgn2_6/ptodata/2/pubpna/us06_new_pub.seq:*
4: /cgn_6/ptodata/2/pubpna/us07_new_pub.seq:*
5: /cgn2_6/ptodata/2/pubpna/us07_pubcomb.seq:*
6: /cgn2_6/ptodata/2/pubpna/pctns_pubcomb.seq:*
7: /cgn2_6/ptodata/2/pubpna/us08_pubcomb.seq:*
8: /cgn2_6/ptodata/2/pubpna/us09_pub_comb.seq:*
9: /cgn2_6/ptodata/2/pubpna/us09_new_pub.seq:*
10: /cgn2_6/ptodata/2/pubpna/us09_pubcomb.seq:*
11: /cgn2_6/ptodata/2/pubpna/us10_new_pub.seq:*
12: /cgn2_6/ptodata/2/pubpna/us10_pubcomb.seq:*
13: /cgn2_6/ptodata/2/pubpna/us10_new_pub.seq:*
14: /cgn2_6/ptodata/2/pubpna/us10_pubcomb.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2124	94.7	2143	10 US-09-410-194-16
2	1952.2	87.0	2045	10 US-09-410-194-16
3	849.6	37.9	2452	10 US-09-410-194-18
4	813.6	36.3	2770	9 US-10-09-005-021-1
5	731.8	32.6	1190	10 US-09-410-194-14
c 6	307.6	13.7	490	10 US-09-833-381-336
c 7	276	12.3	437	10 US-09-864-761-3120
c 8	259.8	11.6	430	10 US-09-864-761-1769
c 9	223.8	10.0	227	10 US-09-864-761-18522
c 10	213	9.5	389	10 US-09-783-590-0424
c 11	177	7.9	177	10 US-09-864-161-19899
c 12	175	7.8	22484	10 US-09-875-114-2
c 13	175	7.8	22484	10 US-09-880-107-3341
c 14	174.8	7.8	737	9 US-10-092-154-2001
c 15	174.8	7.8	737	10 US-09-764-847-2001
c 16	174.8	7.8	737	10 US-09-764-847-2001
c 17	174.6	7.8	1545	10 US-09-764-877-3171
c 18	174.6	7.8	32185	10 US-09-764-877-3171
c 19	173.8	7.7	465237	10 US-09-933-267A-1

Sequence	Start	End	Length	Score	DB ID	Length
Sequence 244, APP	173.6	7.7	14962	9	US-10-079-854-244	10
Sequence 244, APP	173.6	7.7	14962	10	US-09-764-878-194	10
Sequence 1367, APP	173.4	7.7	16281	9	US-10-092-154-1367	9
Sequence 1368, APP	173.4	7.7	16285	9	US-10-092-154-1368	9
Sequence 1368, APP	173.4	7.7	16285	10	US-09-764-847-1368	10
Sequence 1369, APP	173.4	7.7	16285	10	US-09-764-847-1369	10
Sequence 2327, APP	172.6	7.7	7960	9	US-10-091-504-2227	9
Sequence 2327, APP	172.6	7.7	32176	9	US-10-091-504-1933	9
Sequence 54, APP	171.6	7.7	1373	9	US-09-974-897-54	10
Sequence 3, APP1	171.6	7.7	1515	10	US-09-822-860-3	10
Sequence 2326, APP	171.6	7.7	17239	9	US-10-091-504-2226	9
Sequence 3, APP1	171.4	7.6	26657	10	US-09-810-673A-3	10
Sequence 1953, APP	171.4	7.6	32176	10	US-09-764-869-1953	10
Sequence 1953, APP	171.4	7.6	32178	9	US-10-091-504-1954	9
Sequence 1954, APP	171.4	7.6	32178	10	US-09-764-869-1954	10
Sequence 1599, APP	171.2	7.6	17792	9	US-10-091-504-1959	9
Sequence 3, APP1	171.2	7.6	24707	9	US-10-274-368-3	9
Sequence 3, APP1	171.2	7.6	24707	10	US-09-740-327-3	10
Sequence 3, APP1	171	7.6	10283	9	US-09-938-79A-3	9
Sequence 3, APP1	171	7.6	38374	10	US-09-880-107-463	10
Sequence 5, APP1	170.6	7.6	41907	10	US-09-967-013-5	10

#### ALIGNMENTS

RESULT	1	US-09-410-194-16
RESULT	16	US-09-410-194-16
PATENT NO.	US20050100A1	Application US/09410194
GENERAL INFORMATION:		
APPLICANT:	Tschopp, Jurg	
APPLICANT:	Burns, Kimberly	
APPLICANT:	Timmer, Marten	
APPLICANT:	Hahne, Michael	
APPLICANT:	Schröter, Michael	
APPLICANT:	Schneider, Pascal	
APPLICANT:	Bodmer, Jean-Luc	
APPLICANT:	Steiner, Veronique	
APPLICANT:	Rimoldi, Donata	
APPLICANT:	Hofmann, Ray	
APPLICANT:	French, E. Lars	
TITLE OF INVENTION:	FLIP GENES AND FLIP PROTEINS	
FILE REFERENCE:	11.141-02001	
CURRENT APPLICATION NUMBER:	US/09/410,194	
PRIOR APPLICATION NUMBER:	PCT/EP98/01857	
PRIOR APPLICATION NUMBER:	US/09-03-31	
PRIOR APPLICATION NUMBER:	GERMANY 197 13 393.2	
PRIOR APPLICATION NUMBER:	1997-04-01	
SOFTWARE: FastSEQ for Windows Version 4.0		
SEQ ID NO 16		
PRIOR FILING DATE:	1998-03-31	
PRIOR FILING DATE:	1997-04-01	
CURRENT FILING DATE:	1999-09-30	
LENGTH:	2143	
TYPE: DNA		
ORGANISM: Homo sapiens		
FEATURE:		
NAME/KEY: CDS		
LOCATION: (383)...(1822)		
US-09-410-194-16		

Qy	99 TAGGGTGGGGACTCGGCCCTACACAGTGAGTCGGCTATTGGACATTGTCAGTGCAC 158
Matches 2139, Conservative	99.7%
Indels 5, Gaps 1;	

Db	1	TAGGGTGGGACTCGGCCAACACAGTAGTGGACTCCGGATTGGACTTTGTCAAGTGAC	60	Qy	1239	TCTGCCTGATAATGGATGGCATGGCAATGAGAGACAGACCTTCACCT	1298
Qy	159	AGCTGAGAACACAGGACCAAGGAGCTGGAGAGTGTGGAGAGAAGCAGCCGAACAGGCAT	218	Db	1140	TCTGCCTGATAATGGATGGCATGGCAATGAGAGACAGACCTTCACCT	1199
Qy	61	AGCTGAGAACACAGGACCAAGGAGCTGGAGAGTGTGGAGAGAAGCAGCCGAACAGGCAT	120	Db	1200	CCCTGGCTGATAATGGATGGCATGGCAATGAGAGACAGACCTTCACCT	1358
Db	219	GCCCCAGCACCAAGTTCGGTTCAGGCTTCAGGCTTCAGGCTTCAGGCTTCAGGCT	278	Db	1200	CCCTGGCTGATAATGGATGGCATGGCAATGAGAGACAGACCTTCACCT	1259
Qy	121	GCCCCAGCACCAAGTTCGGTTCAGGCTTCAGGCTTCAGGCTTCAGGCTTCAGGCT	180	Qy	1359	TGGCCAAATTGGCTGTAGTGGAGAAATTCTTCAGTATGGATGTTATCCCAGATT	1418
Db	279	TCCCGGGCCTCTAGGGAGCCGGTCAAGCTGGAGAGTGGCGGAGAAGCAGCA	338	Db	1260	TTGSCCAATTGGCTGTAGTGGCCAGACCCGAGATAGCAGCTTGTGTCCTGG	1319
Qy	181	TCCCGGGCCTCTAGGGAGCCGGTCAAGCTGGAGAGTGGCGGAGAAGCAGCA	240	Qy	1419	TGACCCGAGGGTCCCAAGAGTGTATGGTGTAGTGGAGACTCACTCAGGGCTCCCC	1478
Qy	339	GGACCRACCTCCCACTGGAGGATTCTGAANGAAATTCAAGCAGCCCTCAAGAATGA	398	Db	1320	TGACCCGAGGGTCCCAAGAGTGTATGGTGTAGTGGAGACTCACTCAGGGCTCCCC	1379
Db	241	GGACCAACTCCCCACTGAAAGGATTCTGAAGAATTAAGTCAGCCTCAAGAATGA	300	Qy	1479	TGCATCACATCAGGGAGGTTCATGGAGATTCATGGAGATTCATGGAGGAGGCCAA	1538
Qy	399	GTTGACTGCTGCTGGCTCTCTGGTGAATGGCCGGACACTGACTGCAAGACCCCTGTG	458	Db	1380	TGCATCACATCAGGGAGGTTCATGGAGGATTCATGGAGGATTCATGGAGGAGGCCAA	1439
Db	301	GTTGACTGCTGCTGGCTCTGGTGAATGGCCGGACACTGACTGCAAGACCCCTGTG	359	Qy	1539	AGATGTTTTTATTCAGAARCTATGGCTCAGGGATGAAAGATGTGAAATTCAGGAGCCCT	1598
Qy	459	AGCTTCCCTAGTCTTAAAGAATGGCTGGTCAAGTGGATCTTGTGCTTATAGATGTG	518	Db	1440	AGATGTTTTTATTCAGAARCTATGGCTCAGGGAGCTGGATGGAGAGCCCT	1499
Db	360	AGCTTCCCTAGTCTTAAAGAATGGCTGGTCAAGTGGATCTTGTGCTTATAGATGTG	419	Qy	1599	TGGAGGTGGATGGCAGGGATGAAAGATGTGAAATTCAGGCTCAGAAGGGAGGGCTGT	1658
Qy	519	TTGATACAGATGAGAGGAGATGGCTGGTCTTGTGCTGAGTCTTCAGGTGTCAGG	578	Db	1500	TGGAGGTGGATGGCAGGGATGAAAGATGTGAAATTCAGGCTCAGAAGGGAGGGCTGT	1539
Db	420	TTGATACAGATGAGAGGAGATGGCTGGTCTTGTGCTGAGTCTTCAGGTGTCAGG	479	Qy	1659	GCACGTTACCGAGAAGCTGACTPCTTCTGGACCTGTGACTGGAATGTGCTGC	1718
Qy	579	TTCCACCTTAAGTCAGGGACCCTTCGGATATTTCAGGGAAAGGGTAAGCTGTCTGTG	638	Db	1560	GCACGTTACCGAGAAGCTGACTPCTTCTGGACCTGTGACTTGTGACTGCGCATGTCCTG	1619
Db	480	TTCCACCTTAAGTCAGGGACCCTTCGGATATTTCAGGGAAAGGGTAAGCTGTCTGTG	539	Qy	1719	TGGACACAGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGAC	1778
Qy	639	GGACTTGGCTGAACTGCTCTACAGAGTAGGGATTGGCTCAACGTTCTGTA	698	Db	1620	TGGACACAGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGAC	1679
Db	540	GGGACTTGGCTGAACTGCTCTACAGAGTAGGGATTGGCTCAACGTTCTGTA	599	Qy	1779	AAGAAGAAAACGGCACAATCTGCTGAAATCTTCACATGTAACCTGATGTT	1838
Qy	699	AGATGGACAGAAAAGCTGTGGAGACCCACCTGCTCAGGAAACCTTCAGGCT	758	Db	1680	AAGAAGAAAACGGCACAATCTGCTGAAATCTTCACATGTAACCTGATGTT	1739
Db	600	AGATGGACAGAAAAGCTGTGGAGACCCACCTGCTCAGGAAACCTTCAGGCT	659	Qy	1839	GGAAAGCAGCTGCTGGGAGGAATATTATGCTGGCTGAGCACACTCTGAGAA	1898
Qy	759	ATAGAGTGTGCTGATGGCAAGAGATTGGTGTGAAATCTGATGTCCTCATTA	818	Db	1740	GGAAACAGACAGTTCTGGCAAGGGAAATATTATGCTGGCTGAGCACACTCTGAGAA	1799
Db	660	ATAGAGTGTGCTGATGGCAAGAGATTGGTGTGAAATCTGATGTCCTCATTA	719	Qy	1899	AGAAACTTATCTCTACATGAAAGCTGGGGTAGGGCTCAACCT	1958
Qy	819	TTCCTCTATGAGGATTACATGGGGAGCAAGTAACTCAAGGAGAGTTCTGG	878	Db	1800	AGAAACTTATCTCTACATGAAAGCTGGGGTAGGGCTCAACCT	1839
Db	720	TTCCTCTATGAGGATTACATGGGGAGCAAGTAACTCAAGGAGAGTTCTGG	779	Qy	1959	GTAACTCCAGCAGCTGGGGAGCAAGGGCAGATCACTTCAGTCAGGTGTCAG	2018
Qy	879	ACCTTGTGTTGTTGAGTGGAGAAACTAAATTGGTGTGCCAGATAACTGGATTATTAG	938	Db	1860	GTAACTCCAGCAGCTGGGGAGCAAGGGCAGATCACTTCAGTCAGGTGTCAG	1919
Db	780	ACCTTGTGTTGAGTGGAGAAACTAAATTGGTGTGCCAGATAACTGGATTATTAG	839	Qy	2019	CCAGGCTGGCCAACCTGGTAAACGGCTTAACTTAACTGGGAGCTGTCAGT	2078
Qy	939	AAAATCTAAAGAACATCCACAGATAACCTGAGAACAAATTCCAGAGTAAAGC	998	Db	1920	CCAGGCTGGCCAACCTGGTAAACGGCTTAACTTAACTGGGAGCTGTCAGT	1979
Db	840	AAAATGCTAAAGAACATCCACAGATAACCTGAGAACAAATTCCAGAGTAAAGC	899	Qy	2079	GGTGTGGGACCTGTTCCAGTACTTGGGAGCTGAGTGGGAGCTTGTGAC	2138
Qy	999	AGTCCTGTTCAAGGAGCAAGTGTACAGGAAATGTTCTCAAGCAGCAATCCAAAGA	1058	Db	1980	GGTGTGGGACCTGTTCCAGTACTTGGGAGCTGAGTGGGAGCTTGTGAC	2039
Db	900	AGTCCTGTTCAAGGAGCAAGTGTACAGGAAATGTTCTCAAGCAGCAATCCAAAGA	959	Qy	2139	CCAGGAGTTCAAGGCTCATAGATGCTGATGTTGCTGAGTAACTGATAACCAA	2138
Qy	1059	GTCTCAAGGATCTCAATAACTCAGGCTCCATATGGAGAACTTAAGAACAAAGC	1118	Db	2040	CCAGGAGTTCAAGGCTCATAGATGCTGATGTTGCTGAGTAACTGATAACCAA	2099
Db	960	GTCTCAAGGATCTCAATAACTCAGGCTCCATATGGAGAACTTAAGAACAAAGC	1019	Qy	2199	CCTGGCCAATATAAGCAAGATCCCATCTTAACTGGGAGCTTAACTGGGAG	2242
Qy	1119	TAAAGGACACGTTGGCTCAACAGAAACCTGAGAACATGGAAATCCATGAGA	1178	Db	2100	CCTGGCCAATATAAGCAAGATCCCATCTTAACTGGGAGCTTAACTGGGAG	2143
Db	1020	TAAAGGACACGTTGGCTCAACAGAAACCTGAGAACATGGAAATCCATGAGA	1079				
Qy	1179	CTTTTTCCTCAAGGCTACCTGAGAGGATACAGATGAGAGCAAGGCCCTAGGAA	1238				
Db	1080	CTTTTTCCTCAAGGCTACCTGAGAGGATACAGATGAGAGCAAGGCCCTAGGAA	1139				

RESULT\_2  
US-09-861-270-1  
; Sequence 1, Application US/09861210

Patent No. US20020052474A1  
 GENERAL INFORMATION:  
 APPLICANT: Sui, Hong-Bing  
 INVENTOR: Goeddel, David V.  
 TITLE OF INVENTION: Regulators of Apoptosis  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Science & Technology Law Group  
 STREET: 75 Denise Drive  
 CITY: Hillsborough  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94010  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.3.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/861,270  
 FILING DATE: 18-May-2001  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/795,088  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Osman, Richard A.  
 REGISTRATION NUMBER: 36,627  
 REFERENCE/DOCKET NUMBER: T97-001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 343-4341  
 TELEFAX: (650) 343-4342  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2045 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-861,270-1

Query Match 87 0%; Score 1952 2; DB 10; Length 2045;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1965; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 48 GCGACCTTGAGCTTCACCGAGACTCACTAAAGGACTCCGGACTAGGGTGTG 107  
 Db 78 GAGAGCTTGAGCTTCACCGAGACTCACTAAAGGACTCCGGAGCTAGGGTGTG 137  
 Qy 108 GGACTCGGCCCTCACAGTAGTGCGGCCATTGGACTTTGTCAGTGAGAC 167  
 Db 138 GGACTCGGCCCTCACAGTAGTGCGGCCATTGGACTTTGTCAGTGAGAC 197  
 Qy 168 AACAGGGACCAAGGAGGGTGTAGGAGAGAACGGCCAGGCCAGCAC 227  
 Db 198 AACAGGGACCAAGGAGGGTGTAGGAGAGAACGGCCAGGCCAGCAC 257

Qy 228 CAAGTCGGCTTCAGGCTTGCGGTTCTGCCTTCATGTTGGCTGGCTCCGGGT 287  
 Db 258 CAAGTCGGCTTCAGGCTTGCGGTTCTGCCTTCATGTTGGCTGGCTCCGGGT 317  
 Qy 288 CTAGGGGAGGAAGGCTGAAGTGGCAGGGCAGGAGACCGGGCAGGAGACT 347  
 Db 318 CTAGGGGAGGAAGGCTGAAGTGGCAGGGCAGGAGACCGGGCAGGAGACT 377  
 Qy 348 CCCCCACTGAAAGGATTCTGAAAGAAATGAAGTCAAGCTCAGAAATGAGTGA 407  
 Db 378 CCCCCACTGAAAGGATTCTGAAAGAAATGAAGTCAAGCTCAGAAATGAGTGA 437

Qy 408 CTGCTGGCTTCCMGTGACTGGCCGGAGCTGTAATGAGCTGACTCCCT 467  
 Db 438 CTGCTGGCTTCCMGTGACTGGCCGGAGCTGTAATGAGCTGACTCCCT 496

Qy 468 AGTCTAAGAGTAGGATGCTGCTGCTGAAGTCATCCATCAGGGTGAAGAACACTTGATGAG 527  
 Db 497 AGTCTAAGAGTAGGATGCTGCTGCTGAAGTCATCCATCAGGGTGAAGAACACTTGATGAG 556  
 Qy 528 ATGAGAAGGAGATGCTGCTTGTGCCGGATGTGCTCATGATGTGGTTCACCTA 587  
 Db 557 ATGAGAAGGAGATGCTGCTTGTGCCGGATGTGCTCATGATGTGGTTCACCTA 616  
 Qy 588 ATGAGAAGGACCTCTGGATATTACGGAAAGGTAAGCTGTGCTGGGACTPG 647  
 Db 617 ATGAGAAGGACCTCTGGATATTACGGAAAGGTAAGCTGTGCTGGGACTPG 676  
 Qy 648 CTGAACTGCTCAGAGTGAGGGATTGACCTGCTAACCTATCTGAAGATGGACA 707  
 Db 677 CTGAACTGCTCAGAGTGAGGGATTGACCTGCTAACCTATCTGAAGATGGACA 736  
 Qy 708 GAAAAGCTTGAGAACCCACCTGCTCAGGAACCCCTACCTTGTTCGGACTATAGAGTGC 767  
 Db 737 GAAAAGCTTGAGAACCCACCTGCTCAGGAACCCCTACCTTGTTCGGACTATAGAGTGC 796  
 Qy 768 TGATGCCAGAGATGCTGAGGATTGGATAATCTGATGTGCTCAGTAATTFFCCCTA 827  
 Db 797 TGATGCCAGAGATGCTGAGGATTGGATAATCTGATGTGCTCAGTAATTFFCCCTA 856  
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 Db 857 TGAGGATACATGGCCAGGCTGAGTAATGGCTGGCCACATCACTGGATTATTAGAAATAATGCC 947  
 Qy 888 TTGAGTTGGAAACTTAATTGGTGTGCCACATCACTGGATTATTAGAAATAATGCC 947  
 Db 917 TTGAGTTGGAAACTTAATCTGATGTGCCACATCACTGGATTATTAGAAATAATGCC 976  
 Qy 948 TAAGGACATCCACAGANTAGACCTGAGCAGCARAATCCAGAAGTACAGCAGTCGTC 1007  
 Db 977 TAAGGACATCCACAGANTAGACCTGAGCAGCARAATCCAGAAGTACAGCAGTCGTC 1036  
 Qy 1008 AAGGNAGGGAGGAGGTACAGGATGTCAGGATGTCAGGATGTCAGGATGTCAGG 1067  
 Db 1037 AAGGAGCAGGGAGGAGGTACAGGATGTCAGGATGTCAGGATGTCAGGATGTCAGG 1096  
 Qy 1068 ATCCCTCAAAATAACTTCAGGCTCCATAATGGGAGAAAGACAAGACTTAAGGAC 1127  
 Db 1097 ATCCCTCAAAATAACTTCAGGCTCCATAATGGGAGAAAGACAAGACTTAAGGAC 1156  
 Qy 1128 AGCTTGGCTTCACAAAGAACCTGAGAAACCATCAGGAAATCAGAACCTTTTGC 1187  
 Db 1157 AGCTTGGCTTCACAAAGAACCTGAGAAACCATCAGGAAATCAGAACCTTTTGC 1216  
 Qy 1188 CTCAGAGCATACCTGAGAGGATAAAAGTGAAGAGGATAAAAGTGAAGAGCCTAGGAATCTGCCNGA 1247  
 Db 1217 CTCAGAGCATACCTGAGAGGATAAAAGTGAAGAGGATAAAAGTGAAGAGCCTAGGAATCTGCCNGA 1276  
 Qy 1248 TAATGATGCTGATGCTGAGCTTGAGACGCTTCTGAGACCTTCACCTCCCTGGCT 1307  
 Db 1277 TAATGATGCTGATGCTGAGACGCTTCTGAGACCTTCACCTCCCTGGCT 1336  
 Qy 1308 ATGAGATGCCAAATTCTGCATCATGATGCCAGATTCTGCCCAT 1367  
 Db 1337 ATGAGTCCGAAATTCTGCTCATGATGCCAGATTCTGCCCAT 1396  
 Qy 1368 TTGCTGTATGCCAGACGAGACTAGACAGCTTGTGTTCTGGTGAAGCCGAG 1427  
 Db 1397 TTGCTGTATGCCAGACGAGACTAGACAGCTTGTGTTCTGGTGAAGCCGAG 1456  
 Qy 1428 GAGCTCCCAGAGTGTGATGGTGGATCAGACTCAGGGCTCCCCCTGCATCACA 1487  
 Db 1457 GAGCTCCCAGAGTGTGATGGTGGATCAGACTCAGGGCTCCCCCTGCATCACA 1516  
 Qy 1488 TCAGGGAGTAGTGTCAAGGAGATCAGGGCTTATCTAGCAGGGAAAGCCAAGGATGTTT 1547  
 Db 1517 TCAGGGAGTAGTGTCAAGGAGATCAGGGCTTATCTAGCAGGGAAAGCCAAGGATGTTT 1576







RESULT 7  
US-09-380-546a-1.rnpb

SEQUENCE 3120, Application US/09864761  
Patient No. US2002048763A1

GENERAL INFORMATION:  
 APPLICANT: Penn, Sharron G.  
 APPLICANT: Rank, David R.  
 APPLICANT: Hanzel, David K.  
 APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 FILE REFERENCE: Aeonica-X-1

CURRENT APPLICATION NUMBER: US/09/09864761  
 CURRENT FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: US 60/180,312  
 PRIOR FILING DATE: 2000-02-04  
 PRIOR APPLICATION NUMBER: US 60/207,456  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: US 09/632,366  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: GB 24263.6  
 PRIOR FILING DATE: 2000-10-04  
 PRIOR APPLICATION NUMBER: US 60/236,359  
 PRIOR FILING DATE: 2000-09-27  
 PRIOR APPLICATION NUMBER: PCT/US01/00666  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00664  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00663  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00662  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00661  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00670  
 PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687  
 PRIOR FILING DATE: 2000-09-21  
 PRIOR APPLICATION NUMBER: US 09/608,408  
 PRIOR FILING DATE: 2000-06-30  
 PRIOR APPLICATION NUMBER: US 09/774,203  
 PRIOR FILING DATE: 2001-01-29  
 NUMBER OF SEQ ID NOS: 4917  
 SOFTWARE: Adnomax Sequence Listing Engine vers. 1.1  
 SEQ ID NO: 3120  
 LENGTH: 437  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: MAP TO AC007272.2  
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5  
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8  
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2  
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1  
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.9  
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3  
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.5  
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.6  
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.5  
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2  
 US-09-864-761-3120

Query Match Score 12.3%; Score 276; DB 10; Length 437;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-78;  
 Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 487 TCCCTGAACTGCATCCATCGGTGAGAACACTGTACATGAGAAAGATGTCAGGGACCTTCTCTGG 546  
 Db 437 TGCTGAAGTCATCCATCGGTGAGAACACTGTACATGAGAAAGATGTCAGGGACCTTCTCTGG 378

Qy 547 CTTTTTGCGGGATGTGCTATAGATGTTGCTACGGTTGAGAGCACTTGTACAGATGAGAAAGATGTCAGGGACCTTCTCTGG 606  
 Db 377 CTTTTGCGGGATGTGCTATAGATGTTGCTACGGTTGAGAGCACTTGTACATGAGAAAGATGTCAGGGACCTTCTCTGG 318

Qy 607 TATTATCGGAAAGAGGTAAGCTGCTGCTGAGCTGGGACTGTGGCTGAAGCTGTCTACAGATG 666  
 Db 317 TATTATCGGAAAGAGGTAAGCTGCTGCTGAGCTGGGACTGTGGCTGAAGCTGTCTACAGATG 258

Qy 667 GAGGCCATTGACCTGCTGCAAGCTGTGGCTGAAGCTGTGGACCCCA 726  
 Db 257 GAGGCCATTGACCTGCTGCAAGCTGTGGCTGAAGCTGTGGACCCCA 198

Qy 727 CCTGCTCAGGAACCCCTCACCTGTGGCACTATAG 762  
 Db 197 CCTGCTCAGGAACCCCTCACCTGTGGCACTATAG 162

RESULT 8  
US-09-864-761-1769/c  
 Sequence 1769, Application US/09864761  
 Patent No. US2002048763A1  
 GENERAL INFORMATION:  
 APPLICANT: Penn, Sharron G.  
 APPLICANT: Rank, David R.  
 APPLICANT: Hanzel, David K.  
 APPLICANT: Chen, Wensheng  
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 FILE REFERENCE: Aeonica-X-1  
 CURRENT APPLICATION NUMBER: US/09/09864761  
 CURRENT FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: US 60/180,312  
 PRIOR FILING DATE: 2000-02-04  
 PRIOR APPLICATION NUMBER: US 60/207,456  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: US 09/632,366  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: GB 24263.6  
 PRIOR FILING DATE: 2000-10-04  
 PRIOR APPLICATION NUMBER: US 60/236,359  
 PRIOR FILING DATE: 2000-09-27  
 PRIOR APPLICATION NUMBER: PCT/US01/00666  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00664  
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 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00661  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00670  
 PRIOR FILING DATE: 2001-01-30

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 FILE REFERENCE: Aeonica-X-1  
 CURRENT APPLICATION NUMBER: US/09/09864761  
 CURRENT FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: PCT/US01/0048763A1  
 PRIOR FILING DATE: 2000-02-04  
 PRIOR APPLICATION NUMBER: US 60/180,312  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: US 09/632,366  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: GB 24263.6  
 PRIOR FILING DATE: 2000-10-04

APPLICANT: Rank, David R.  
 APPLICANT: Hanzel, David K.  
 APPLICANT: Chen, Wensheng  
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 FILE REFERENCE: Aeonica-X-1  
 CURRENT APPLICATION NUMBER: US/09/09864761  
 CURRENT FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: PCT/US01/0048763A1  
 PRIOR FILING DATE: 2000-02-04  
 PRIOR APPLICATION NUMBER: US 60/180,312  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: US 09/632,366  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: GB 24263.6  
 PRIOR FILING DATE: 2000-10-04

RESULT 9  
US-09-864-761-18522/C  
Sequence 18522, Application US/09864761  
; Patient No. US2002048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanezel, David K.  
; APPLICANT: Chen, Wenshang  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aeonimica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annotrax Sequence Listing Engine vers. 1.1  
SEQ ID NO: 1769  
LENGTH: 430  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
; OTHER INFORMATION: MAP TO AC007283.3  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.1  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.8  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.4  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.6  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.9  
US-09-864-761-1769  
Query Match 11.6%; Score 259.8; DB 10; Length 430;  
Best Local Similarity 97.4%; Pred. No. 2.1-e-73; Indels 0; Gaps 0;  
Matches 264; Conservative 0; Mismatches 7; Gaps 0;  
  
Qy 1524. TAGCAGGAAGCCAAGATGTTTATTCAACTATGTGGTCAAGGGCCAGCTGG 1583  
Db 430 TAGCAGGAAGCCAAGATGTTTATTCAACTATGTGGTCAAGGGCCAGCTGG 371  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
; OTHER INFORMATION: MAP TO AC007283.3  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.1  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.8  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.6  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.9  
; OTHER INFORMATION: EXPRESSED IN EST\_HUMAN HIT: AF113952.4, VALUE 1.00e-122  
; OTHER INFORMATION: EXPRESSED IN NT HIT: AF015450.1, VALUE 1.00e-125  
; OTHER INFORMATION: SWISSPROT HIT: P96254, VALUE 6.60e+00  
  
Qy 1584 AGAACAGCAGCCCTCTGGAGCTGTGGACAGTTCACCGAGCTGACTCTCTGGAGCCCTGTACTG 1643  
Db 370 AGAACAGCAGCCCTCTGGAGCTGTGGACAGTTCACCGAGCTGACTCTGGAGCCCTGTACTG 311  
  
Qy 1644 AGAAGCCAGGGCTGTGGACAGTTCACCGAGCTGACTCTCTGGAGCCCTGTACTG 1703  
Db 310 AGAAGCCAGGGCTGTGGACAGTTCACCGAGCTGACTCTCTGGAGCCCTGTACTG 251  
  
Qy 1704 CGGACATGTCCTGTGGACAGTTCACCGAGCTGACTCTGGAGCCCTGTACTGAGTC 1763  
Db 250 CGGACATGTCCTGTGGACAGTTCACCGAGCTGACTCTGGAGCCCTGTACTGAGTC 191  
  
Qy 1764 CCCGAAACTGAGACAAGAAAAGAACGCC 1794  
Db 190 CCCGAAACTGAGACAAGAAAAGAACGCC 160

Query Match 10.0%; Score 223.8; DB 10; Length 227;  
 Best Local Similarity 99.1%; Pred. No. 6.1e-62;  
 Matches 225; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1556 AACTATGCTGTGTCAGGGCCAGCTGGAAACAGCCTCTGGGGATGGGCCA 1615  
 Db 227 AACTATGCTGTGTCAGGGCCAGCTGGGGATGGGCCA 168

Qy 1616 GGATGAAAGAATGGAAATCAAGGCTGAAACGGCTGACAGTCACCGAGA 1675  
 Db 167 GGATGAAAGAATGGAAATCAAGGCTGAAACGGCTGACAGTCACCGAGA 108

Qy 1676 GCTGACTCTTCTGAGCTGTACTCGGACATGTCCTGGACAGCTCACAGC 1735  
 Db 107 GCTGACTCTTCTGAGCTGTACTCGGACATGTCCTGGACAGCTCACAGC 48

Qy 1736 TCACCGTCCCTGACTCTGAGCTGCCTCTCCAGAAACTGAGACAAGA 1782  
 Db 47 TCACCATCCCTGACTCTGAGCTGCCTCCAGAAACTGAGACAAGA 1

RESULT 10

Sequence 4424, Application US/09783590  
 GENERAL INFORMATION:  
 APPLICANT: Dillon, Patrick J.  
 APPLICANT: Hassaine, William A.  
 APPLICANT: Li, Haodong  
 APPLICANT: Rosen, Craig A.  
 APPLICANT: Ruben, Steven M.  
 TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2  
 FILE REFERENCE: PO-16.2C1  
 CURRENT APPLICATION NUMBER: US/09/7783,590  
 PRIOR FILING DATE: 2000-02-15  
 PRIOR APPLICATION NUMBER: 08/420,856  
 PRIOR FILING DATE: 1994-11-21  
 NUMBER OF SEQ ID NOS: 12485  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 4424  
 LENGTH: 389  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1)  
 OTHER INFORMATION: n equals a,t,g, or c  
 LOCATION: (15)  
 OTHER INFORMATION: n equals a,t,g, or c  
 NAME/KEY: misc feature  
 LOCATION: (115)  
 OTHER INFORMATION: n equals a,t,g, or c  
 NAME/KEY: misc feature  
 LOCATION: (282)  
 OTHER INFORMATION: n equals a,t,g, or c  
 NAME/KEY: misc feature  
 LOCATION: (318)  
 OTHER INFORMATION: n equals a,t,g, or c  
 NAME/KEY: misc feature  
 LOCATION: (335)  
 OTHER INFORMATION: n equals a,t,g, or c  
 NAME/KEY: misc feature  
 LOCATION: (353)  
 OTHER INFORMATION: n equals a,t,g, or c  
 NAME/KEY: misc feature  
 LOCATION: (356)  
 OTHER INFORMATION: n equals a,t,g, or c  
 NAME/KEY: misc feature  
 LOCATION: (362)  
 OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: misc feature  
; LOCATION: (364)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (374)  
; OTHER INFORMATION: n equals a,t,g, or c  
; US-09-783-590-4424

Query Match 9.5%; Score 213; DB 10; Length 389;  
 Best Local Similarity 93.2%; Pred. No. 2.7e-58;  
 Matches 287; Conservative 0; Mismatches 13; Indels 8; Gaps 6;

Qy 1053 AAAGACTCTCAGGATCCTTCATAATCTAGGGCTCATATGGGAAGATAAAC 1112  
 Db 14 ANAGAGCTCAGGCTTCATAATCTAGGGCTCATATGGGAAGATAAAC 73

Qy 1113 AAAGACTTAAGGAAACGCTGGGCTAACAAAGAACCGATG-AAGAAATCCATTAGGAA 1171  
 Db 74 AAAGACTTAAGGAAACGCTGGGCTAACAAAGAACCGATGNAAGAAATCCATTAGGAA 133

Qy 1172 TCAGAAGCTTTTGCTTCAGAGCATACCTGAGAGGATAGAAGGAAAGGCC 1231  
 Db 134 TCAGAAGCTTTTGCTTCAGAGCATACCTGAGAGGATACAAGTGAAGGAAAGGCC 193

Qy 1232 CTA-GGAACTCGCTGAT-AATCGATGCTTCATGCTTC-GAGA 1287  
 Db 194 CTAGGAACTCGCTGATGAAATCGATGCTTCATGAACTGAGCTTCGGGAA 253

Qy 1268 CACCTTCACTTCCCTGGCTATGAA--GTCCGAATTCTGCATCTCAGTATGCATGG 1344  
 Db 254 CACCTTCACTTCCCTGGCTATGAAATTCGCATCTCAGTATGCATGG 313

Qy 1345 TATATCCC 1352  
 Db 314 TATTNTCC 321

RESULT 11  
 US-09-864-761-19899/C  
 Sequence 1989, Application US/09864761  
 Patent No. US20020048763A1  
 GENERAL INFORMATION:  
 APPLICANT: Penn, Sharron G.  
 APPLICANT: Rank, David R.  
 APPLICANT: Hanzel, David K.  
 APPLICANT: Chen, Wensheng  
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
 FILE REFERENCE: AeonBio-X-1  
 CURRENT APPLICATION NUMBER: US/09/864,761  
 CURRENT FILING DATE: 2001-05-23  
 PRIORITY NUMBER: US 60/160,312  
 PRIOR FILING DATE: 2000-02-04  
 PRIORITY NUMBER: US 60/207,456  
 PRIOR FILING DATE: 2000-05-26  
 PRIORITY NUMBER: US 09/632,366  
 PRIOR FILING DATE: 2000-08-03  
 PRIORITY NUMBER: GB 24252,6  
 PRIOR FILING DATE: 2000-10-04  
 PRIORITY NUMBER: US 60/236,359  
 PRIOR FILING DATE: 2001-09-27  
 PRIORITY NUMBER: PCT/US01/00666  
 PRIOR FILING DATE: 2001-01-30  
 PRIORITY NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIORITY NUMBER: PCT/US01/00664  
 PRIOR FILING DATE: 2001-01-30  
 PRIORITY NUMBER: PCT/US01/00669  
 PRIOR FILING DATE: 2001-01-30  
 PRIORITY NUMBER: PCT/US01/00665  
 PRIOR FILING DATE: 2001-01-30  
 PRIORITY NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1  
; SEQ ID NO: 19899  
; LENGTH: 177  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC007272.2  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1  
; OTHER INFORMATION: EXPRESSED IN HB100, SIGNAL = 1.9  
; OTHER INFORMATION: EXPRESSED IN HEA, SIGNAL = 3.3  
; OTHER INFORMATION: EXPRESSED IN BT74, SIGNAL = 3.5  
; OTHER INFORMATION: EXPRESSED IN FEPAL LIVER, SIGNAL = 2.6  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5  
; OTHER INFORMATION: SWISSPROT HIT: O51391, EVALU 4.90e+00  
; OTHER INFORMATION: EST\_HUMAN HIT: AW691851.1, EVALU 3.00e-95  
; OTHER INFORMATION: NT HIT: AF015450.1, EVALU 2.00e-95  
; US-09-864-761-19899

Query Match 7.9%; Score 177; DB 10; Length 177;  
Best Local Similarity 100.0%; Pred. No. 6.9e-47;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 482 ATGTCGTGAAAGTCATCAGTTGAGAACATTGATACAGATAAGAGATG 541  
Db 177 ATGTCGTGAAAGTCATCAGTTGAGAACATTGATACAGATAAGAGATG 118

Qy 542 CTGCCTTGTGCGGGATGTGCTCATAGATGTGTCACCTTAATCTAGGACCT 601  
Db 117 CTGCCTTGTGCGGGATGTGCTCATAGATGTGTCACCTTAATCTAGGACCT 58

Qy 602 CTGGATATTTACGGAAAGAGTAAGCTGAAGCTGCGGGAAGTGCGTCACRGCTC 658  
Db 57 CTGGATATTTACGGAAAGAGTAAGCTGAAGCTGCGGGAAGTGCGTCACRGCTC 1

RESULT 13  
US-09-880-107-3341/C  
; Sequence 3341, Application US/09880107  
; Patent No. US2002142981A1

GENERAL INFORMATION:  
; APPLICANT: Horne, Darcie T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09-880-107  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 3341  
; LENGTH: 22484  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US2002142981A1 U29953  
; NAME/KEY: unsure  
; LOCATION: (1) (22484)  
; OTHER INFORMATION: n = a or c or g or t  
; US-09-880-107-3341

Query Match 7.8%; Score 175; DB 10; Length 22484;  
Best Local Similarity 76.2%; Pred. No. 7.5e-45;

Qy 1921 ATAGAAACCAAAAGCTGGCGTAGTGGCTCACCCCTGAACTTGGGAGG 1980  
Db 9823 AAAAAAAAAGCAGGGCAAGCTGCTAAACCTGTAATCCACACTTGAGAGG 9764

Query Match 7.8%; Score 175; DB 10; Length 22484;  
Best Local Similarity 76.2%; Pred. No. 7.5e-45;  
Matches 246; Conservative 0; Mismatches 65; Indels 12; Gaps 2;

Qy 1981 CCAAGGAGGGCAGATCAGTCAGTTGAGAACGCTGGCAAATGG-TAA 2039  
Db 9763 CGCGGCGGGTAGATCACCTGAGTCAGAGTGTGAGCCAAATGAGAA 9704

Qy 2040 ACGGCTGCCTCTAGTAATAATGCCAAATTAGCTGGCTGGGTGCTGCTCC 2099  
Db 9703 ACCCCATCTCTACTAAATAACAAATAAGCGGGGTGGGGCATGCCCTGAAVCC 9644

Qy 2100 CAGTACCTGGAGGCTAGGTGGAGGATCTTGAACCCAGGATTCAGGGCTATAGC 2159  
Db 9643 CAGCTACTGGGGCTAAGCGAGGATCATGATCCAGGAATCTGGAGGTGCGATG 9584

Qy 2160 ATGGCTGTGATTGTGCCCTACGAATAACCTGGCAAATAACAGATC 2219  
Db 9583 GAGGTGAGATCG-----CGCACTGCACCTCCAGGTGGCAAGCAGCAAGACT 9535

Qy 2220 CCATCTCTTAAAAAAGAAAAAA 2242  
Db 9534 CCATCTCTAAAAAAGAAAAAA 9512

Matches 246; Conservative 0; Mismatches 65; Indels 12; Gaps 2;

Qy 1921 ATAGAAACCAAAAGGCTGGCGTAGTGGCTCACACTTCCCAGAACACTTGGGAGG 1980  
 Db 9823 AAAAAGAAAAAGGCCAGGGCAGTCGCTCAAACCTGTAATCCACACTTGAGAGG 9764

Qy 1981 CCAAGGGCAGATCACTGAGGCTGGCACATGG-TAA 2039  
 Db 9763 CCGGGGGTAGATCACCTGAGGTGAGCACATCTGGCAACATGGAGA 9704

Qy 2040 ACGETGTCCTAGAAAATGCAAATTAGCTGGTGGTGGCTACCTGTGTC 2099  
 Db 9703 ACCCATCTACTAACATAATTAGCCGGTGGTGGCAGCTGTAATC 9644

Qy 2100 CAGTACTGGAGGTCTGGGAGGTCTTTGAACCCAGGAGTCAGGGTCA TAG 2159  
 Db 9643 CAGCTACTGGAGGCTAGGAGAGTGGAGGTGCACT 9584

Qy 2160 ATGCTGTGATTGGCTTAGAACCTGGCAATATAGCAAGTC 2219  
 Db 9583 GAGCTGAGATCG-----CGCCACTGCACCTCCAGCTGGCAAOAGCAAGACT 9535

Qy 2220 CCATCTTAAATAAAAAA 2242  
 Db 9534 CCATCTCAAAARAAAAAA 9512

Db 5052 AAATAATTACACATAGCCGGCGGGCACACCTGTAAATCCAGCTGGCA 4993

Qy 1919 ACATAAGAACCAAAAGGCTGGGTAGTGGCTCACACCTGTAAATCCAGCTGGCA 1978  
 Db 4992 GGCGAGGGAGGATCACATGGTCAAGGACTTGAGGCTGGCAACAGGTG 4933

Qy 2038 AAAGCTGTCCTAGTAAATGCAAAATTAGCTGGTGGGAGTGGTACCTGGT 2097  
 Db 4932 AAATCCCGTCTCACTAAATGCAAAATTAGCTGGTGGGAGTGGTACCTGGT 4873

Qy 2098 CCCAGTTACTGGAGGTGAGGTGGGAGGATCTTGAAACCCAGAGGTTCAGGTCTA 2157  
 Db 4872 CCAGSATATCTGGGGGTGAGGTGGGAGNTGGCTTAAACCCAGAGGTTCAGGTCTA 4813

Qy 2158 GCATGCTGATTTGCCCTACGATAGCCACTGCAATACCAACCTGGGAAATATAGCAGA 2217  
 Db 4812 GTGAGCCGGAGATG-----AGCCACTGCACTCCAGCTGGCAACAGCGAGA 4764

Qy 2218 TCCCCATCTTAAATAAAAAAA 2243  
 Db 4763 CCCTCATCIAAAACACACACAA 4738

RESULT 15  
 US-09-764-887-453/c  
 Sequence 43; Application US/09764887  
 Patent No. US20042096A1  
 GENERAL INFORMATION:  
 APPLICANT: Rosen et al.  
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 FILE REFERENCE: PA113  
 CURRENT APPLICATION NUMBER: US/09/764 ,887  
 CURRENT FILING DATE: 2001-01-17  
 Prior application data removed - consult PALM or file wrapper  
 NUMBER OF SEQ ID NOS: 658  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 453  
 LENGTH: 7737  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-764-887-453

Query Match 7.8%; Score 174.8; DB 10;  
 Best Local Similarity 75.8%; Pred. No. 4.3e-45;  
 Matches 247; Conservative 0; Mismatches 67; Indels 12; Gaps 2;

Qy 1919 ACATAAGAACCAAAAGGCTGGGTAGTGGCTCACACCTGTAAATCCAGCTGGCA 1978  
 Db 5052 AAATAATTACACATAGCCGGCGGGCACACCTGTAAATCCAGCTGGCA 4993

Qy 1979 GGCGAAGGAGGGAGGATCACTICAGGCTGGAGACTTGAGGCTGGCAACATGGT- 2037  
 Db 4992 GGCGAGGGAGGATCACATGGTCAAGGACTTGAGGCTGGCAACAGGTG 4933

Qy 2038 AAAGCTGTCCTAGTAAATGCAAAATTAGCTGGTGGGAGTGGTACCTGGT 2097  
 Db 4932 AAATCCCGTCTCACTAAATGCAAAATTAGCTGGTGGGAGTGGTACCTGGT 4873

Qy 2098 CCCAGTTACTGGAGGTGAGGTGGGAGGATCTTGAAACCCAGAGGTTCAGGTCTA 2157  
 Db 4872 CCAGSATATCTGGGGGTGAGGTGGGAGNTGGCTTAAACCCAGAGGTTCAGGTCTA 4813

Qy 2158 GCATGCTGATTTGCCCTACGATAGCCACTGCAATACCAACCTGGGAAATATAGCAGA 2217  
 Db 4812 GTGAGCCGGAGATG-----AGCCACTGCACTCCAGCTGGCAACAGCGAGA 4764

Qy 2218 TCCCCATCTTAAATAAAAAAA 2243  
 Db 4763 CCCTCATCIAAAACACACAA 4738

Search completed: April 12, 2003, 22:34:53  
 Job time : 231.706 secs

Matches 247; Conservative 0; Mismatches 65; Indels 12; Gaps 2;

Qy 1919 ACATAAGAACCAAAAGGCTGGGTAGTGGCTCACACCTGTAAATCCAGCTGGCA 1978  
 Db 5052 AAATAATTACACATAGCCGGCGGGCACACCTGTAAATCCAGCTGGCA 4993

Qy 1979 GGCGAAGGAGGGCAGATCACTCAGGTGGGAGGTGAGGCTGAGAACCTGGCAACATGGT- 2037  
 Db 4992 GGCGAGGGAGGATCACATGGTCAAGGACTTGAGGCTGGCAACAGGTG 4933

Qy 2038 CCCAGTTACTGGAGGTGAGGTGGGAGGATCTTGAAACCCAGAGGTTCAGGTCTA 2157  
 Db 4872 CCAGSATATCTGGGGGTGAGGTGGGAGNTGGCTTAAACCCAGAGGTTCAGGTCTA 4813

Qy 2158 GCATGCTGATTTGCCCTACGATAGCCACTGCAATACCAACCTGGGAAATATAGCAGA 2217  
 Db 4812 GTGAGCCGGAGATG-----AGCCACTGCACTCCAGCTGGCAACAGCGAGA 4764

Qy 2218 TCCCCATCTTAAATAAAAAAA 2243  
 Db 4763 CCCTCATCIAAAACACACAA 4738

Result No.	Score	Query Match	Length	DB ID	Description
1	1991	88.8	2040	4	Sequence 33, Appli
2	1952.2	87.0	2045	4	Sequence 1, Appli
3	1619.2	72.2	1750	3	Sequence 1, Appli
4	1619.2	72.2	1750	3	Sequence 1, Appli
5	1619.2	72.2	1750	3	Sequence 1, Appli
c	175	7.8	14581	4	Sequence 4, Appli
c	175	7.8	22481	4	Sequence 43, Appli
c	175	7.8	22484	4	Sequence 43, Appli
c	10	174.8	7.8	17377	1
c	11	170.6	7.6	35060	3
c	12	169.8	7.6	72928	3
c	13	168.4	7.5	38674	4
c	14	168.2	7.5	36741	4
c	15	168.2	7.5	87350	3
c	16	168.2	7.5	87543	4
c	17	167	7.4	2923	1
c	18	167	7.4	2923	2
c	19	167	7.4	2923	4
c	20	167	7.4	29242	4
c	21	166.8	7.4	32042	4
c	22	166.6	7.4	282	1
c	23	166.6	7.4	9704	4
c	24	165.4	7.4	112132	4
c	25	164.8	7.3	36761	4
c	26	164.2	7.3	36651	4
c	27	163.8	7.3	8353	3
c	28	163.8	7.3	43950	4
c	29	163.6	7.3	99500	4
c	30	163.6	7.3	246240	2
c	31	163.6	7.3	246240	2
c	32	163.6	7.3	246240	2
c	33	163.2	7.3	4853	4
c	34	162.8	7.3	3166	4
c	35	162.2	7.2	508	3
c	36	162.2	7.2	508	4
c	37	162.2	7.2	508	4
c	38	162.2	7.2	2396	4
c	39	162	7.2	3627	4
c	40	161.8	7.2	162450	4
c	41	161.8	7.2	246240	2
c	42	161.8	7.2	246240	2
c	43	161.8	7.2	246240	2
c	44	161.4	7.2	6769	1
c	45	161.4	7.2	6769	1

## ALIGNMENTS

RESULT 1  
US-09-069-023-33  
; Sequence 33, Application US/09069023A  
; Patent No. 634873  
; GENERAL INFORMATION:  
; APPLICANT: Inohara, Naohiro  
; APPLICANT: Koski, Takeyoshi  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS  
; FILE REFERENCE: UM-0333  
; CURRENT APPLICATION NUMBER: US/09-069, 023A  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 33  
; LENGTH: 2040  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-069-023-33

## SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.  
Qd is derived by analysis of the total score distribution.

## SUMMARIES

Query Match 88.8%; Score 991; DB 4; Length 2040;  
Best Local Similarity 99.0%; Pred. No. 0; Mismatches 20; Indels 0; Gaps 0;  
Matches 203; Conservative 0; MisMatches 20;

QY 47 AGCGAGCTGCCTCACAGTGTGGCGCTATTGACTTTGTCACTGACGCTGAG 106  
Db 1 AGCGAGCTGCCTCACAGTGTGGCGCTATTGACTTTGTCACTGACGCTGAG 60

QY 107 GGACTCTGCCCTCACAGTGTGGCGCTATTGACTTTGTCACTGACGCTGAG 166  
Db 61 GGACTCTGCCCTCACAGTGTGGCGCTATTGACTTTGTCACTGACGCTGAG 120

QY 167 CAAAGAACCGAGGGAGGGAGGTGAGAGAGGACGGATGCCAGCA 226  
Db 121 CAAAGAACCGAGGGAGGGAGGTGAGAGAGGACGGATGCCAGCA 180

QY 227 CCAAGTCGGCTTCAGGCCTTCGGTTCTCATCTGGTTCGCCCTCCGGCG 286  
Db 181 CCAAGTCGGCTTCAGGCCTTCGGTTCTCATCTGGTTCGCCCTCCGGCG 240

QY 287 TCTAGGGAGGAGGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGC 346  
Db 241 TCTAGGGAGGAGGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGC 300

QY 347 TCCCCACTGGAAAGGATTCTGAAGAAATGAAGTCAAGCCCTCAAGAATGAGTTGACTG 406  
Db 301 TCCCCACTGGAAAGGATTCTGAAGAAATGAAGTCAAGCCCTCAAGAATGAGTTGACTG 360

QY 407 CCTGCTGGCTTCCTGTTGACTGGCCGGAGCTGTACTGCAAGACCTTGAGCTTCCC 466

144.1 ATCAGGAGCATGTPCATGGAGATCATGCCPPTATCPAGCAGGGAAAGCCAACAGTGT 1506  
 Db 361 CCTGCTGGCTTCCTTGACTGGCCGGAACTGACTGCAGACCCCTTGAGCTCCC 420  
 Qy 467 TAGCTAAGAATAGGATGTCGTCGTAAGTCACTGGTGAAGAACGACTTGATA 526  
 Db 421 TAGTCTAAGAATAGGATGTCGTCGTAAGTCACTGGTGAAGAACGACTTGATA 480  
 Db 527 GATGAAAGGAGATGCTGCTTTGTCGCCCCGATGTTGCTATAGTGTGCTGAGTCACTGGTGAAGAACGACTTGATA 586  
 Qy 481 GATGAAAGGAGATGTCGCTTTGTCGCCCCGATGTTGCTATAGTGTGCTGAGTCACTGGTGAAGAACGACTTGATA 540  
 Qy 587 ATGCGAGGACCTCTGGATATTAGCGAAAGAGCTAACGTTACCTGCGGGACTTG 646  
 Db 541 ATATGCGAGGACCTCTGGATATTAGCGAAAGAGCTAACGTTACCTGCGGGACTTG 600  
 Qy 647 GCTGAATCTGCTCACAGAGTGGGGATTCACCTGCTCAACGATCTAACAGTGGAC 706  
 Db 601 GCTGAATCTGCTCACAGAGTGGGGATTCACCTGCTCAACGATCTAACAGTGGAC 660  
 Qy 707 AGAAAAGCTGGAGACCCACCTGCTCACAGAGTGGGGATTCACCTGCTAACAGTGGAC 766  
 Db 661 AGAAAAGCTGGAGACCCACCTGCTCACAGAGTGGGGATTCACCTGCTAACAGTGGAC 720  
 Qy 767 CTGATGGAGATGTTGAGGATTTGATAATCTGATGTTGCTCATPAATTTCTC 826  
 Db 721 CTGATGGAGATGTTGAGGATTTGATAATCTGATGTTGCTCATPAATTTCTC 780  
 Qy 827 ATGAAAGGATTAATGGCCGAGGGCAGATAAGCAAGGAGAGTTCTGACCTTGTG 886  
 Dr .1 ATGAAAGGATTAATGGCCGAGGGCAGATAAGCAAGGAGAGTTCTGACCTTGTG 840  
 Qy 887 GTTGAGTTGGAGAACTTAATTGGSTGCCCCAGATCAACTGGATTATTAGAAAATGC 946  
 Db 841 GTTGAAGTTGGAGAACTTAATTGGTGGCCCTGGATGTTGAGGATTAATPGAAAATGC 900  
 Qy 947 CTAAGAACATCCACAGATTAAGCTGAGCAAAATCAGAAGTAGCAAGGAGATTCGGACCTGT 1006  
 Db 901 CTAAGAACATCCACAGATTAAGCTGAGCAAAATCAGAAGTAGCAAGCAGCTGT 960  
 Qy 1007 CAAGGGAGGGACAGATTAAGGAAATGTTCCAAAGGAAATCAAAGAGTCTCAAG 1066  
 Db 961 CAAGGGAGGGACAGATTAAGGAAATGTTCCAAAGGAAATCAAAGAGTCTCAAG 1020  
 Qy 1067 GATCCPTCAATAAATCTCAGGCTCCATAATGGAGAAGTAAAGAACGCTTAAAGGA 1126  
 Db 1021 GATCCPTCAATAAATCTCAGGCTCCATAATGGAGAAGTAAAGAACGCTTAAAGGA 1080  
 Qy 1127 CAGCTTGGCTCACAGAACGCTGAGAACGCTGAGAACGCTGAGAACGCTGAG 1186  
 Db 1081 CAGCTTGGCTCACAGAACGCTGAGAACGCTGAGAACGCTGAGAACGCTGAG 1140  
 Qy 1187 CCTCAAGCATACCTGAGAGATAAGGAGATAAGGAGATAAGGAGATAAGGAG 1246  
 Db 1141 CCTCAAGCATACCTGAGAGATAAGGAGATAAGGAGATAAGGAGATAAGGAG 1200  
 Qy 1247 ATAATGATGTCATGGCAATGAGAACGACTGAGAACGCTGAGAACGCTGAG 1306  
 Db 1201 ATAATGATGTCATGGCAATGAGAACGACTGAGAACGCTGAGAACGCTGAG 1260  
 Qy 1307 TATGAAGTCAGAACATCTCAGAACGACTGAGAACGACTGAGAACGCTGAG 1366  
 Db 1261 TATGAAGTCAGAACATCTCAGAACGACTGAGAACGACTGAGAACGCTGAG 1320  
 Qy 1367 TTGGCTGTAGGCCAGACCCAGACTGAGAACGACTGAGAACGACTGAGAACG 1426  
 Db 1321 TTGGCTGTAGGCCAGACCCAGACTGAGAACGACTGAGAACGACTGAGAACG 1380  
 Qy 1427 GGAGGCTCCAGAGTGTATGGTGGATGAGAACGACTCAGGGCTCCCTGCACTCAC 1486  
 Db 1381 GGAGGCTCCAGAGTGTATGGTGGATGAGAACGACTCAGGGCTCCCTGCACTCAC 1440  
 Qy 1487 ATCAGGAGGAGTTCTAGGGAGATCATGCCCTATCTAGAGGAGAACGAAAGATGT 1546

Db 144.1 ATCAGGAGCATGTPCATGGAGATCATGCCPPTATCPAGCAGGGAAAGCCAACAGTGT 1506  
 Qy 1547 TTTATCAGAACTATGTTGTCAGAGGGCCAGCTGGACAACAGCAGCTCTGGAGCT 1606  
 Db 1501 TTATCAGAACTATGTTGTCAGAGGGCCAGCTGGACAACAGCAGCTCTGGAGCT 1560  
 Qy 1607 GATGGCCAGGATGAGATGGAATTCAGGCTCAAGGCTTCAGACAGCTGGGGCT 1666  
 Db 1561 GATGGCCAGGATGAGATGGAATTCAGGCTCAAGACAGCTGGGGCT 1620  
 Qy 1667 CACCGAGAAGCTGACTCTCTGAGCCGACATGTCCTGTTGAGCAG 1726  
 Db 1621 CACCGAGAAGCTGACTCTCTGAGCCGACATGTCCTGTTGAGCAG 1680  
 Qy 1727 TCTCACACTCACCGTCCCTGACTCTGAGCTCCAGAACGACTGAGACAGAA 1786  
 Db 1681 TCTCACAGCTCACCATCCCTGAGCTTCACTGGTACATGTTGAGAACGAGC 1740  
 Qy 1787 AACAGCCCACCTCTGATCTCATGGTACACTGGTACATGTTGAGAACGAGC 1846  
 Db 1741 AACAGCCCACCTCTGATCTCATGGTACACTGGTACATGTTGAGAACGAGC 1800  
 Qy 1847 AGATGTTCTGCCAAGGAGAAATTATCTGCTGCCAACCTCTGAGAACGAGA 1906  
 Db 1801 AGATGTTCTGCCAAGGAGAAATTATCTGCTGCCAACCTCTGAGAACGAGA 1860  
 Qy 1907 ATCCCTCTACACATAGAAACCAAAAGGCTGGCAGTCACCTGTAATCCC 1966  
 Db 1861 ATCCCTCTACACATAGAAACCAAAAGGCTGGCAGTCACCTGTAATCCC 1920  
 Qy 1967 AGGACTTGGAGGGCAAGGGGAGATCAGCTCAGGCTGGCTGAGACCCCTG 2026  
 Db 1921 AGGACTTGGAGGGCAAGGGGAGATCAGCTCAGGCTGGCTGAGACCCCTG 1980  
 Qy 2027 GCACACATGGTAAACGCTGTCCTAGTAAAAATGCAAAATA 2069  
 Db 1981 GCACACATGGTAAACGCTGTCCTAGTAAAAATGCAAAATA 2023

RESULT 2  
 US-08-795-0BRA-1  
 Sequence 1, Application US/08795088A  
 Patent No. 6242569  
 GENERAL INFORMATION:  
 APPLICANT: Sui, Hong-Bing  
 ATTORNEY/AGENT: Goeddel, David V.  
 TITLE OF INVENTION: Regulators of Apoptosis  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Science & Technology Law Group  
 STREET: 75 Denise Drive  
 CITY: Hillsborough  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94010  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/795.088A  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Oshain, Richard A.  
 REGISTRATION NUMBER: 36,627  
 REFERENCE/DOCKET NUMBER: T97-001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 343-4341  
 TELEX: (650) 343-4342  
 INVENTORY CHARACTERISTICS:  
 SEQUENCE CHARACTERISTICS:  
 SEQUENCE ID: SEQ ID NO: 1;

LENGTH:	2045 base pairs	Db	977	TAAGAACATCCACAGAATAAGACAAATCCAGAAGTACAAGCAGTCGTGTC 1036
TYPE:	nucleic acid	Qy	1008	AAGGAGCAGGGACAAAGTTACAGGAATGTTCTCCAAGGACATCCAAAAGAGTCCTAAGG 1067
STRANDEDNESS:	double	Db	1037	AAGGGCAGGGACAAAGTTACAGGAATGTTCTCCAAGGACATCCAAAAGAGTCCTAAGG 1096
TOPOLOGY:	linear	Qy	1068	ATCCCTCAATAACTCAGGCTCATATAAGGAAAGAACAAAGACTTAAGGAC 1127
MOLECULE TYPE:	CDNA	Db	1097	ATCCCTCAATAACTCAGGCTCATATAAGGAAAGAACAAAGACTTAAGGAC 1156
US-08-795-088A-1	Matches 1965:保守性 99.8%; Pred. No. 0; Mismatches 0; Gaps 1;	Qy	48	GCGACCTTGAGCCTCACCGACGAGTCMTCAGTAAAGGACATCCGGAGCTAGGGTGC 107
		Db	78	GAGAGCTTSCAGCCTCACCGACGAGTCMCAACTAAAGGACATCCGGAGCTAGGGTGC 137
		Qy	108	GGACTCGGGCTCACAGTAGTCAGTGGCTTGTAACTTACAGGACATCCGGAGCTAGAGA 167
		Db	138	GGACTCGGGCTCACAGTAGTCAGTGGCTTGTAACTTACAGGACATCCGGAGCTAGAGA 197
		Qy	168	AACAGGGACACCGGAGGTAGGAGAAGGAGGTAGGAGAAGCAGCCAGCAC 227
		Db	198	AACAGGGACACCGGAGGTAGGAGAAGGAGGTAGGAGAAGCAGCCAGCAC 257
		Qy	228	CAAGTCGGCTTCCAGGCTTTCGGTTCTCGCTTCATTTGGTGCCTTCGGCGT 287
		Db	318	CAAGTCGGCTTCCAGGCTTTCGGTTCTCGCTTCATTTGGTGCCTTCGGCGT 317
		Qy	288	CTAGGGGAGGAAGCTGGAGCTGGAGACTGGCCAGGCCAACAGGAC 347
		Db	318	CTAGGGGAGGAAGCTGGAGCTGGAGACTGGCCAGGCCAACAGGAC 377
		Qy	348	CCCCCACTGAAAGGATTCTGAAAGAATGAAACCTCAGAACCTGACTGC 407
		Db	378	CCCCCACTGAAAGGATTCTGAAAGAATGAAACCTCAGAACCTGACTGC 437
		Qy	408	CTGCTGGCTTCCCTGTTGACTGGCCGGAGCTGAGCTTCCCT 467
		Db	438	CTGCTGGCTT-CCTGTTGACTGGCCGGAGCTGAGCTTCCCT 496
Q,		Qy	468	AGCTTAAGACTGGATCTGCTGAGTATCCTAGGGTGLAAACACTGATAGA 527
		Db	497	AGCTTAAGACTGGATCTGCTGAGTATCCTAGGGTGLAAACACTGATAGA 556
		Qy	528	ATGAGAAGGAGATGGCTCTTGTGCGGGATGTTCTATAAGTGGTCCACCTA 587
		Db	557	ATGAGAAGGAGATGGCTCTTGTGCGGGATGTTCTATAAGTGGTCCACCTA 616
		Qy	588	ATGTCAGGGACCTTCCTGGTATTTAACGGGAAGAGGTAAGCTGCTGGGGACTTG 647
		Db	617	ATGTCAGGGACCTTCCTGGTATTTAACGGGAAGAGGTAAGCTGCTGGGGACTTG 676
		Qy	648	CTGACAGCTCTACAGAGTGGGGATTTGGATAATCTGATCTGGCTAACCTGAGATGGCA 707
		Db	677	CTGACAGCTCTACAGAGTGGGGATTTGGATAATCTGATCTGGCTAACCTGAGATGGCA 736
		Qy	708	GAAAAGCTGGAGACCCACCTGCTCAGAACCCCTCACCTTGTGGACTATAGACTGC 767
		Db	737	GAAAAGCTGGAGACCCACCTGCTCAGAACCCCTCACCTTGTGGACTATAGACTGC 796
		Qy	768	TGATGGCAAGATGGTGGGGATTGGATAATCTGATCTGGCTCATTAATTTCCTCA 827
		Db	797	TGATGGCAAGATGGTGGGGATTGGATAATCTGATCTGGCTCATTAATTTCCTCA 856
		Qy	828	TGAGGATTAATGGCCAGGGAGATAGAGGAGATAGAGGAGATAGAGGAGATAGAGT 887
		Db	857	TGAGGATTAATGGCCAGGGAGATAGAGGAGATAGAGGAGATAGAGGAGATAGAGT 916
		Qy	888	TGAGGATTAATGGCCAGGGAGATAGAGGAGATAGAGGAGATAGAGGAGATAGAGT 947
		Db	917	TGAGGATTAATGGCCAGGGAGATAGAGGAGATAGAGGAGATAGAGGAGATAGAGT 976
		Qy	948	TAAGAACATCCACAGAATAAGACCTGAGACAAAAATCCAGAAGTACAAGCAGTCGTGTC 1007

Sequence 1, Application US/08859167		Db	360	GGCCGGAGCTGTACTGCAAGACCCCTGGAGCTCCTAGTCAAGTAGGTGCTG	419
GENERAL INFORMATION:		Qy	489	CTGAAGTCATCCATAGGTGAAGAGCACTTGATACTAGATGAGAGATGCTGCCT	548
Patent No. 6037461		Db	420	CTGAAGTCATCCATAGGTGAAGAGCACTTGATACTAGATGAGAGATGCTGCCT	479
APPLICANT: Almamri, Emad S.		Qy	549	TTTCTGCGGGATTTGCTATAGATGCTGCCACCTATGTCAGGACCTCTGGATA	608
APPLICANT: Fernandez-Almamri, Teresa		Db	480	TTTTCTGCGGGATTTGCTATAGATGCTGCCACCTATGTCAGGACCTCTGGATA	539
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF		Qy	609	TTTACGGAAAGAGTAAGCTGCTGACTGCTACAGAGTA	668
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS		Db	540	TTTACGGAAAGAGTAAGCTGCTGACTGCTACAGAGTA	599
NUMBER OF SEQUENCES: 17		Qy	669	GGGATTGACCTGGCAACGTAACGTTGAGATGACAGAACGCTGTGAGACCCAC	728
CORRESPONDENCE ADDRESS:		Db	600	GGCATTGACCTGGCAACGTAACGTTGAGATGACAGAACGCTGTGAGACCCAC	659
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461ris		Qy	729	TGCTAGGACCCCTACCTTGCGACTATAGTCGAGATGCTGAGATGCTGAGG	788
STREET: One Liberty Place, 46th floor		Db	660	TGCTAGGACCCCTACCTTGCGACTATAGTCGAGATGCTGAGATGCTGAGG	719
CITY: Philadelphia		Qy	789	ATTGGATAAATCTGATGCTGCTTAAATTCTCATGAGGTTACATGGCCAG	848
STATE: PA		Db	720	ATTGGATAAATCTGATGCTGCTTAAATTCTCATGAGGTTACATGGCCAG	779
ZIP: 19103		Qy	849	GCAAGATAACCAAGGAGAGAGTTCTGACCTTGCGTTGACTTGAGAAACTAAIT	908
COMPUTER READABLE FORM:		Db	780	GCAGATGCTGAGGAGAGAGTTCTGACCTTGCGTTGACTTGAGAAACTAAIT	839
MEDIUM TYPE: Floppy disk		Qy	909	TGGTGCCTTCAAGATCACTGGATTATTAGAAAATGCCAACTCACAGAATP	968
COMPUTER: IBM PC compatible		Db	840	TGGTGCCTTCAAGATCACTGGATTATTAGAAAATGCCAACTCACAGAATP	899
OPERATING SYSTEM: WINDOWS		Db	960	ACCTGAGAACAAATCCAGAAACTACAAGCAGTCTGTTCAAGGAGCAGTTACA	1028
SOFTWARE: WordPerfect		Qy	900	ACCTGAGAACAAATCCAGAAACTACAAGCAGTCTGTTCAAGGAGCAGTTACA	959
CURRENT APPLICATION DATA:		Db	1029	GGATGTTCTCAACGCAATCCAAAGCTCAAGATCTTCAATAACTCTAGGC	1088
APPLICATION NUMBER: US/08/859,167		Db	960	GGATGTTCTCAACGCAATCCAAAGCTCAAGATCTTCAATAACTCTAGGC	1017
FILING DATE:		Qy	1089	TCCATAATGGAGAGTAAAGAACGTTAAAGAACAGCTTGGCTCAACAGAAC	1148
CLASSIFICATION: 435		Db	1018	- - - - -	1017
NAME/AGENT/ATTORNEY/AGENT INFORMATION:		Qy	1149	CAGTGAAGAAATCCATTAGGAATCAGAACCTACCTGAGAGA	1208
NAME: Deluca, Mark		Db	1018	- - - - -	- - - - -
REGISTRATION NUMBER: 33,229		Qy	1209	GATAGAGATGAAAGGCAAGCCCCTAGGAACTCTGCTGATAATGCTGCAATG	1268
RECEIVER/DOCKET NUMBER: TJSU-		Db	1035	GATAGAGATGAAAGGCAAGCCCCTAGGAACTCTGCTGATAATGCTGCAATG	1094
RECOMMUNICATION INFORMATION:		Qy	1269	AGACAGAGCTCTGAGACACCTTCACTTCCCTGGTATGAGTCCAGAAATTCTG	1328
TELEPHONE: (215) 568-3100		Db	1095	AGACAGAGCTCTGAGACACCTTCACTTCCCTGGTATGAGTCCAGAAATTCTG	1154
TELEFAX: (215) 568-3439		Qy	1329	ATCAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG	1388
INFORMATION FOR SEQ ID NO: 1:		Db	1155	ATCAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG	1214
SEQUENCE CHARACTERISTICS:		Qy	1389	GAGCTTGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1448
LENGTH: 1750 base pairs		Db	1215	GAGACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1274
TYPE: nucleic acid		Qy	1449	GTGCGATCAGACTAGGGCTCCCTGATCACATCAGGAGTCTGGGAG	1508
STRANDEDNESS: double		Db	1275	GTGCGATCAGACTAGGGCTCCCTGATCACATCAGGAGTCTGGGAG	1334
TOPOLOGY: both		Qy	1509	ATTATGCCCTTATGCTGAGCTTAACTGAGTGTGCTGATGCTG	1568
MOLECULE TYPE: cDNA		Qy	429	GGCCGGAGCTGTACTGCAAGACCCCTGGCTGAGCTTCCAGAGCTGCTG	488
FEATURE:					
NAME/KEY: CDS					
LOCATION: 413..1750					
US-08-859-167-1					

1335	ATTATGCCCTTATCAGGGAGCCAAAGTGTTTTATCAGAACATGTGGTGT 1394
1569	CAGGGCCAGCTGGAGAACAGCGCCCTTGTGGAGCTGGATGGCCAGCGATGAAATG 1628
1395	CAGGGCCAGCTGGAGCACGGCCCTTGTGGATGGCCAGCGATGAAATG 1454
1629	TGGATTTCAGGGCTCAAGGGAGGGCTGTGCACAGTACCCAGAACGTCAGCTCT 1688
1455	TGGATTTCAGGGCTCAAGGGAGGGCTGTGCACAGTACCCAGAACGTCAGCTCT 1514
1689	GGACCTGTGTACTGGGACATGCTCCGTGAGCACTCAGAGTCACCGTCCTGT 1748
1515	GGACCTGTGTACTGGACATGCTCCGTGAGCACTCAGAGTCACCGTCCTGT 1574
1749	ACCTGAGTGGCCCTCCAGAAACTGAGACAAGAAAGAAAAGCCCACTCTGGATCTC 1808
1575	ACCTGAGTGGCCCTCCAGAAACTGAGACAAGAAAGAAAAGCCCACTCTGGATCTC 1634
1809	ACATTTGAACCTCAATGGTACATGTGATGTTGGAAACAGGAGTGTCTGCCAAGGAAAT 1868
1635	ACATTTGAACCTCAATGGTACATGTGATGTTGGAAACAGGAGTGTCTGCCAAGGAAAT 1694
1869	ATTATGCTGGCTGGAGCACACTCTGAGAAAGAACATCTCTCTACACATA 1924
1695	ATTATGCTGGCTGGAGCACACTCTGAGAAAGAACATCTCTCTACACATA 1750

SUITE 4  
-09-109-273-1

Sequence 1, Application US/09109273  
Patent No. 6063760

**GENERAL INFORMATION:**

APPLICANT: Almeli, Enad S.  
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF  
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS  
TITLE OF INVENTION: OF MAKING THE SAME

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760ris  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: WINDOWS  
SOFTWARE: WordPerfect

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/109, 273  
FILING DATE:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/859, 167  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: DeLuca, Mark  
REGISTRATION NUMBER: 33, 229  
REFERENCE/DOCKET NUMBER: TUU-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1750 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE: CDS  
NAME/KEY:

Qy	69	CGAGTCTCACTAAAGG	72	GTGGCGGCATATTGGACAT
Db	1	CGAGTCTCACTAAAGG		
Qy	129	GTAGGAGAACGGCC		
Db	61	GTGGCGGCATATTGGACAT		
Qy	189	TGAGGAGAACGGCC		
Db	121	TGTTGAGAACGGCC		
Qy	249	GGTTCTTGCTTCATC		
Db	181	GGTTCTTGCTTCATC		
Qy	309	TGGCACCGCCAGGAGT		
Db	241	TGGCACCGCCAGGAGT		
Qy	369	AAAGAATGAAGTCGCC		
Db	301	AAAGAATGAAGTCGCC		
Qy	429	GGCCGGAGCTGTACTGCC		
Db	360	GGCCGGAGCTGTACTGCC		
Qy	489	CTGAAGTCTCCATCAGG		
Db	420	CTGAAGTCTCCATCAGG		
Qy	549	TTTGTGGGGATGTGTT		
Db	480	TTTGTGGGGATGTGTT		
Qy	609	TTTACGGAAAGGGTAA		
Db	540	TTTACGGAAAGGGTAA		
Qy	669	GCGATTTACCTCTCA		
Db	600	GCGATTTACCTCTCA		
Qy	729	TGCTAGGACACCCTCAC		
Db	660	TGCTAGGACACCCTCAC		
Qy	789	ATTGGATAAATCTGTG		
Db	720	ATTGGATAAATCTGTG		
Qy	849	GCAAGATTAAGCAGAGA		
Db	780	GCAAGATTAAGCAGAGA		
Qy	909	TGGTGCCTCAGATCAAC		
Db	840	TGGTGCCTCAGATCAAC		
Qy	969	ACCTGAAGCAAAATCC		
Db	900	ACCTGAAGCAAAATCC		
Qy	1029	GGAAATGTTCCAGAGA		

CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: Windows  
 SOFTWARE: WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/276, 993  
 FILING DATE: 09/09/2001  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/859, 167  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DeLuca, Mark  
 REGISTRATION NUMBER: 33, 229  
 REFERENCE/DOCKET NUMBER: TUU-  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-3100  
 TELEFAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1750 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: both  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 413 .. 1750  
 US-09-276-993-1

Query Match 72, 28; Score 1619, 2; DB 4; Length 1750;  
 Best Local Similarity 94.1%; Pred. No. 0;  
 Matches 1747; Conservative 0; Indels 106; Gaps 3; Mismatches 1;

Qy	69	CGAGCTCACTAAAGGACTCCGGAGCTAGGGTGGGGACTCGGCCTCACACAGTA 128
Db	1	CGAGTCACATGGGTTGGGAGCTGGGGGTGGGGACTCGGCCTCACACAGTA 60
Qy	129	GTTGGAGAGANGGCCAGCCAGCTGGGCTTGGGAGCTGGGGAGCTGGGGAGGG 188
Db	61	GTTGGGGTATGGCATGGGAGCTGGGGAGCTGGGGAGCTGGGGAGGG 120
Qy	189	GTTGGCTTGGCTCAGCTGGGAGCTGGGGAGCTGGGGAGCTGGGGAGGG 248
Db	121	TGTTAGAGAGAACGCCGGCAAGCAGATGGGGAGCTGGGGAGGG 180
Qy	249	GTTTCTTGGCTCAGCTGGGGAGCTGGGGAGCTGGGGAGGG 308
Db	181	GTTTCTTGGCTCAGCTGGGGAGCTGGGGAGCTGGGGAGGG 240
Qy	309	TGGCAGGGAGCTGACTGAAAGCTGGGGAGCTGGGGAGCTGGGGAGGG 368
Db	241	TGGCAGGGAGCTGACTGAAAGCTGGGGAGCTGGGGAGGG 300
Qy	369	AAGGAATGAACTGAGCTGGGGAGCTGGGGAGCTGGGGAGGG 428
Db	301	AAGGAATGAACTGAGCTGGGGAGCTGGGGAGGG 359
Qy	429	GGCCGGAGCTGACTGAAAGCTGGGGAGCTGGGGAGGG 488
Db	360	GGCCGGAGCTGACTGAAAGCTGGGGAGCTGGGGAGGG 419
Qy	489	CAGAATGATCCATGGGAGCTGGGGAGCTGACTGAAAGCTGGGGAGGG 548
Db	420	CAGAATGATCCATGGGAGCTGACTGAAAGCTGGGGAGGG 479
Qy	549	TGGTGGGGAGCTGACTGAAAGCTGGGGAGCTGGGGAGGG 608

**RESULT 5**  
 Sequence 1, Application US/09/276993  
 Patent No. 6207801  
 GENERAL INFORMATION:  
 APPLICANT: Alnemri, Emad S.  
 ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No., 6207801r  
 STREET: One Liberty Place, 46th floor  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: Windows  
 SOFTWARE: WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/276, 993  
 FILING DATE: 09/09/2001  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/859, 167  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DeLuca, Mark  
 REGISTRATION NUMBER: 33, 229  
 REFERENCE/DOCKET NUMBER: TUU-  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-3100  
 TELEFAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1750 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: both  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 413 .. 1750  
 US-09-276-993-1

Query Match 72, 28; Score 1619, 2; DB 4; Length 1750;  
 Best Local Similarity 94.1%; Pred. No. 0;  
 Matches 1747; Conservative 0; Indels 106; Gaps 3; Mismatches 1;

Qy	1395	CAGAGGCCAGCTGGGAGACAGCAGCTGGGAGCTGGGAGCAATG 1454
Qy	1629	TGGAATTCAAGGCTCAGAGGAGGCTGACAGTCACCGAGAGCTGACTCTCT 1688
Qy	1455	TGGAATTCAAGGCTCAGAGGAGGCTGACAGTCACCGAGAGCTGACTCTCT 1514
Qy	1689	GGAGGCTGTACTCTCCAGAAACTGAGACAGCTGGGGAGCTGGGGAGGG 1748
Qy	1515	GGAGGCTGTACTCTCCAGAAACTGAGACAGCTGGGGAGCTGGGGAGGG 1634
Qy	1749	ACCTGCACTGACCTGGCTCAGAAACTGAGACAGAAAGAAACGCCAACCTGGGATCTTC 1808
Qy	1575	ACCTGCACTGACCTGGCTCAGAAACTGAGACAGAAAGAAACGCCAACCTGGGATCTTC 1634
Qy	1809	ACATTGAACTCTGGCTACATGTATGATGGAAAGAAACTTATCCTCTACACATAA 1868
Qy	1635	ACATTGAACTCTGGCTACATGTATGATGGAAAGAAACTTATCCTCTACACATAA 1750
Qy	1869	ATTATGTTGGTGTGAGCAACTCTGAGAAAGAAACTTATCCTCTACACATAA 1924
Qy	1695	ATTATGTTGGTGTGAGCAACTCTGAGAAAGAAACTTATCCTCTACACATAA 1750

**RESULT 5**  
 Sequence 1, Application US/09/276993  
 Patent No. 6207801  
 GENERAL INFORMATION:  
 APPLICANT: Fernandez-Alnemri, Teresa  
 TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF  
 TREATING CANCER AND METHODS OF TREATMENT  
 TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS  
 TITLE OF INVENTION: OF MAKING THE SAME  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 STREET: One Liberty Place, 46th floor  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: Windows  
 SOFTWARE: WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/276, 993  
 FILING DATE: 09/09/2001  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/859, 167  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DeLuca, Mark  
 REGISTRATION NUMBER: 33, 229  
 REFERENCE/DOCKET NUMBER: TUU-  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-3100  
 TELEFAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1750 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: both  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 413 .. 1750  
 US-09-276-993-1

Query Match 72, 28; Score 1619, 2; DB 4; Length 1750;  
 Best Local Similarity 94.1%; Pred. No. 0;  
 Matches 1747; Conservative 0; Indels 106; Gaps 3; Mismatches 1;

Qy	1395	CAGAGGCCAGCTGGGAGACAGCAGCTGGGAGCTGGGAGCAATG 1454
Qy	1629	TGGAATTCAAGGCTCAGAGGAGGCTGACAGTCACCGAGAGCTGACTCTCT 1688
Qy	1455	TGGAATTCAAGGCTCAGAGGAGGCTGACAGTCACCGAGAGCTGACTCTCT 1514
Qy	1689	GGAGGCTGTACTCTCCAGAAACTGAGACAGAAAGAAACGCCAACCTGGGATCTTC 1808
Qy	1515	GGAGGCTGTACTCTCCAGAAACTGAGACAGAAAGAAACGCCAACCTGGGATCTTC 1634
Qy	1749	ACCTGCACTGACCTGGCTCAGAAACTGAGACAGAAAGAAACGCCAACCTGGGATCTTC 1808
Qy	1575	ACCTGCACTGACCTGGCTCAGAAACTGAGACAGAAAGAAACGCCAACCTGGGATCTTC 1634
Qy	1809	ACATTGAACTCTGGCTACATGTATGATGGAAAGAAACTTATCCTCTACACATAA 1868
Qy	1635	ACATTGAACTCTGGCTACATGTATGATGGAAAGAAACTTATCCTCTACACATAA 1750
Qy	1869	ATTATGTTGGTGTGAGCAACTCTGAGAAAGAAACTTATCCTCTACACATAA 1924
Qy	1695	ATTATGTTGGTGTGAGCAACTCTGAGAAAGAAACTTATCCTCTACACATAA 1750



RESULT 7

US-08-367-841A-43/C  
 Sequence 43, Application US/08367841A  
 Patent No. 6319667  
 GENERAL INFORMATION:  
 APPLICANT: Chader, Gerald J.; Rodriguez, Ignacio R.; Mazuruk, Krzyztof;  
 APPLICANT: Tombran-Tink, Joyce  
 TITLE OF INVENTION: PIGMENT EPITHELIUM  
 TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC  
 TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE  
 NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Morgan & Finnegan  
 STREET: 345 Park Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10154

COMPUTER READABLE FORM:  
 COMPUTER TYPE: FLOPPY DISK  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/367, 841A  
 FILING DATE: 30-DEC-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION NUMBER:  
 APPLICATION NUMBER: 08/257, 963  
 FILING DATE: 07-JUN-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/952, 796  
 FILING DATE: 24-SEP-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DOROTHY R. AUTH  
 REGISTRATION NUMBER: 36434  
 REFERENCE/DOCKET NUMBER: 20264126US2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 758-4800  
 TELEFAX: (212) 751-6849  
 INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 22481 Base Pairs  
 TYPE: Nucleic Acid  
 STRANDEDNESS: Double  
 TOPOLOGY: Unknown  
 MOLECULE TYPE: Genomic DNA  
 FEATURE:  
 NAME/KEY: P1-147  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION: full length genomic sequence for PEDF plus flanking sequences

US-08-367-841A-43

Query Match Score 175; DB 4; Length 22481;  
 Best Local Similarity 76.2%; Pred. No. 1.9e-42;  
 Matches 246; Conservative 0; Mismatches 65; Indels 12; Gaps 2;

Qy 1921 ATAGAAACCCAAAAGCTGCGTGTGGCTAACCTGACTTTGGAGG\_1910  
 Db 9823 AAAAAGGGCAAGGCAGGCAACCTGTAATCCGACTTTGGAGG 9764

Qy 1981 CCAGGAGGGCACATCACTTCAGGTCAAGGTTGGACCCACATGG-TAA 2039  
 Db 9763 CCAGGAGGGTAGATCACCTGGCAACATGGAGAATCTGGCAACATGGAGAA 9704

Qy 2040 ACCGTGCGCTAAATAATGCCAAATTAGCTGGTGGCTACCTGTGTC 2099  
 Db 9703 ACCCATCTCTACTAAATAACAAATAATAGCCGCTGATGCCATGTCATCC 9644

Qy 2100 CAGTACTGGAGGCTGGAGGATCTTGAACCCAGGATTCAGGGTCATPGC 2159  
 Db 9643 CAGCTACTGGGGCTAGGAGATCACTGAACTGGAGTTGAGTTGAGT 9584

Qy 2160 ATGCTGTGATTGNGCTACGAATAGCCACTGATACCCACCGGGAAATAATGCCAAGATC 2219  
 Db 9583 GAGCTGAGTCG-----GCCACTGACTCCAGGCTGGCACAGGCAAGACT 9535

Qy 2220 CCATCTCTTAAAAAAAGAAAAA 2242  
 Db 9534 CCATCTCTCAAAGAAAAAAAGAAAAA 9512

RESULT 8

PCT-US95-07201-43/C  
 Sequence 43, Application PC/TUS9507201  
 GENERAL INFORMATION:  
 APPLICANT: Chader, Gerald J.; Becerra, Sofia  
 APPLICANT: Patricia; Schwartz, Joan P.;  
 APPLICANT: Taniwaki, Takayuki  
 TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC  
 TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Morgan & Finnegan, L.L.P.  
 STREET: 345 Park Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10154  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy Disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WORDPERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/07201  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/367, 841  
 FILING DATE: 30-DEC-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/257, 963  
 FILING DATE: 07-JUN-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/952, 796  
 FILING DATE: 24-SEP-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DOROTHY R. AUTH  
 REGISTRATION NUMBER: 36434  
 REFERENCE/DOCKET NUMBER: 20264126US2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 758-4800  
 TELEFAX: (212) 751-6849  
 INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 22481 Base Pairs  
 TYPE: Nucleic Acid  
 STRANDEDNESS: Double  
 TOPOLOGY: Unknown  
 MOLECULE TYPE: Genomic DNA  
 FEATURE:  
 NAME/KEY: P1-147  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION: full length genomic sequence for PEDF plus flanking sequences

US-08-367-841A-43

Query Match Score 175; DB 4; Length 22481;  
 Best Local Similarity 76.2%; Pred. No. 1.9e-42;  
 Matches 246; Conservative 0; Mismatches 65; Indels 12; Gaps 2;

Qy 1921 ATAGAAACCCAAAAGCTGCGTGTGGCTAACCTGACTTTGGAGG\_1910  
 Db 9823 AAAAAGGGCAAGGCAGGCAACCTGTAATCCGACTTTGGAGG 9764

INFORMATION FOR SEQ ID NO: 43:

REFERENCE/DOCKET NUMBER: 20264126PCT  
 TELECOMMUNICATION INFORMATION:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 22481 Base Pairs  
 TYPE: Nucleic Acid  
 STRANDEDNESS: Double  
 TOPOLOGY: Unknown  
 MOLECULE TYPE: Genomic DNA  
 FEATURE:  
 NAME/KEY: P1-147

LOCATION:	IDENTIFICATION METHOD:
; OTHER INFORMATION: full length genomic sequence for PEDF plus flanking sequences.	PCT-US95-07201-43
Query Match 7.8%; Score 175; DB 5; Length 22481;	
Best Local Similarity 76.2%; Pred. No. 1.9e-42;	
Matches 246; Conservative 0; Mismatches 65; Indels 12; C	
QY 1921 ATAGAACCAAAAGGCTGGGTAGTGGCTCACACCTGTATCCAGCAGACTTGGGAGGG	
Db 9823 AAAAAGAAAAAGGCGAGGGCAGTGCTAAACCTGTATCCAGCAGACTTGGAGGC	
QY 1981 CCAGGAGGCCAGATCACTTCAGTCAGAGTTGAGACAGCAGCTGGCCACATGG-TAT	
Db 9763 CCCAGGGCGGTAGATCACCTGTAGGTAGACATCTGGCATCTGGCCACATGGAGAA	
Qy 2040 ACCGTGCTCTAGTAATAATGCCAAAATTAGTGGGTGGGTGGTGGTACCTGTCTCC	
Db 9703 ACCCCATCTACTAAATAATAGCAAAATTAAGCCGGTGTGGGCATGCTGTATCC	
Qy 2100 CAGTACTTGGAGGCTGAGGTGGAGGATCTTTGAAACCCAGACTTACGGTCATAGG	
Db 9643 CAGCTACTGGAGGCTTGGAGGAACTCACTGATCCAGGAATGGAGGTGGAGGTGCA	
Qy 2160 ATGCTGTGATTTGGCCCTACGAATAGCCACTGCATACCAACCTGGGAAATATAGCAAGATG	
Db 9583 GAGCTGATCTG-----CGCCACTGCACCTCCAGCTGGCAACAGCAAGCA	
Qy 2220 CCATCTTTAAAGAAAAAAA 2242	
Db 9534 CCATCTCAAAGAAAAAAA 9512	
RESULT 9	US-09-875-223-2/C
; Sequence 2, Application US/09875223	
; Patent No. 6391850	
; GENERAL INFORMATION:	
; APPLICANT: NO. 6391850thwestern University	
; APPLICANT: David Dawson	
; APPLICANT: Paul Gillis	
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Angiogenesis	
; FILE REFERENCE: 0290-2303	
; CURRENT APPLICATION NUMBER: US/09/875,223	
; CURRENT FILING DATE: 2001-06-06	
; PRIOR APPLICATION NUMBER: US 09/122,079	
; PRIOR FILING DATE: 1998-07-23	
; PRIOR APPLICATION NUMBER: PCT/US98/115228	
; PRIOR FILING DATE: 1998-07-23	
; PRIOR APPLICATION NUMBER: US 08/899,304	
; PRIOR FILING DATE: 1997-07-23	
; NUMBER OF SEQ ID NOS: 2	
; SOFTWARE: PatentIn Ver. 2.1	
; SEQ ID NO 2	
; LENGTH: 22484	
; TYPE: DNA	
; ORGANISM: Homo sapiens	
; FEATURE:	
; NAME/KEY: Unsure	
; LOCATION: 1..22484	
; OTHER INFORMATION: "n" means either a, c, t, or g	
US-09-875-223-2	
Query Match 7.8%; Score 175; DB 4; Length 22484;	
Best Local Similarity 76.2%; Pred. No. 1.9e-42;	
Matches 246; Conservative 0; Mismatches 65; Indels 12; C	
Qy 1921 ATAGAACCAAAAGGCTGGGTAGTGGCTCACACCTGTATCCAGCAGACTTGGAGGG	
Db 9823 AAAAAGAAAAAGGCGAGGGCAGTGCTAAACCTGTATCCAGCAGACTTGGAGGC	

TOPOLGY: linear  
 MOLECULE TYPE: DNA  
 FEATURE: exon  
 NAME/KEY: exon  
 LOCATION: 621..753  
 FEATURE: intron  
 NAME/KEY: intron  
 LOCATION: 754..9596  
 FEATURE: exon  
 NAME/KEY: exon  
 LOCATION: 9597..9744  
 FEATURE: intron  
 NAME/KEY: intron  
 LOCATION: 9745..16396  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: 16397..17327  
 US-07-9068-871-15

Query Match      7.8%; Score 174.8; DB 1; Length 17327;  
 Best Local Similarity 77.7%; Pred. No. 1.9e-42;  
 Matches 241; Conservative 0; Mismatches 57; Indels 12; Gaps 2;

---

Qy 1935 GGCCTGGCCTAGTGGCTCACACCTGTAAATCCAGCACTTGGGAGGGCAGA 1994  
 Db 7531 GGCGGGTGTGGCTCACACCTGTAAATCCAGCACTTGGGAGACTGAGGGTGA 7590

Qy 1995 TCACTTCAGTCAGAGTGTGAGACCAGTCCAGCAATATGTGT- AAACGCTGCCAATGCT 2053  
 Db 7591 TCACCTGAGGTAGAGTGTGAGACCAGCCTGGCAAACTCCATCCCTACT 7650

Qy 2054 AAAATGCAAAAATTAGTGCGGTGGTGGTACCTGTGTCCCAAGTTACTTGGGA 2113  
 Db 7651 AAAATAAACAAATTAGTGTGGATGATGATGTTGGCACCTGTCTCCAGCTACTGGGA 7710

Qy 2114 GCTGAGGTGGAGGATCTTTGAACCCCAGGGTCAAGGTCAATAGCATGCTGTGATGTG 2173  
 Db 7711 GCTGAGGCAAGAGAATCGGTGAGCCAGCCTGGCAAACTGGTGAAGCCGAGATGT- 7769

Qy 2174 CCTAGGAATGAGCCACTGATCCAACTCTGGCAATATACCAAGATCCCTCTTAAAA 2233  
 Db 7770 -----GCGACTGATCCAGGGCAACAGAGCAAGACTCTCATCTCAAAAAA 7819

Qy 2234 AAAAAAAA 2243  
 Db 7820 AAAAAAAA 7829

RESULT 11  
 US-08-814-095-7  
 Sequence 7, Application US/08814095  
 Patent No. 6025183  
 GENERAL INFORMATION:  
 APPLICANT: Soresh, Hermona  
 APPLICANT: Zakut, Haim  
 APPLICANT: Shani, Moshe  
 TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: KOHN & ASSOCIATES  
 STREET: 30500 No. 6025183thwestern Highway, Suite 410  
 CITY: Farmington Hills  
 STATE: Michigan  
 COUNTRY: U.S.  
 ZIP: 48334  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/814,095

OTHER INFORMATION: /gene= "ACHE"  
 OTHER INFORMATION: /number= 6  
 FEATURE:  
 NAME/KEY: terminator  
 LOCATION: 28129..28131  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: complement (34528..34895)  
 OTHER INFORMATION: /function= "arsenite resistance"  
 OTHER INFORMATION: gene  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 6  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: complement (34092..34358)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 1  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: complement (33779..33963)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 3  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: complement (33493..33591)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 4  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: complement (33297..33408)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 5  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: complement (32959..33094)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 6  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: complement (32328..32528)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 7  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: complement (323386..32468)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 8  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: complement (31894..32080)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 9  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: complement (31363..31534)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 10  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: complement (31131..31284)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 11  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: complement (30816..31011)  
 OTHER INFORMATION: /gene= "AR"  
 OTHER INFORMATION: /number= 12  
 FEATURE:



RESULT 15

US-08-781-891-79

Sequence 79, Application US/08781891

Patent No. 6030620

GENERAL INFORMATION:

APPLICANT: Fu, Ying-Hui  
APPLICANT: Yu, Chang-En  
APPLICANT: Oshima, Junko  
APPLICANT: Mulligan, John T.  
APPLICANT: Scheinfeld, Gerald D.

TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO  
NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:  
ADDRESSEE: SPEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,891  
FILING DATE: 27-DEC-1996  
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: No. 6030620enburg Ph.D., Carol  
REFERENCE/DOCKET NUMBER: 39-317  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 79:

SEQUENCE CHARACTERISTICS:  
LENGTH: 87350 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-781-891-79

Query Match 7.5%; Score 168.2; DB 3; Length 87350;  
Best Local Similarity 75.8%; Pred. No. 5e-40;  
Matches 238; Conservative 0; Mismatches 64; Indels 12; Gaps 2;

Qy 1931 AAAGGCCTGGCTGACTGGCAACCTGTAAATCCAGCACTTGGGAGGCCAAGAGGG 1990  
Db 41980 AAAAACCTGGCATGGACTGGCTACGGCTGTAAATCCAGCACTTGGGAGGCCAAGAGGG 42039

Qy 1991 CAGATCACTCGGGCAAGGACTTCGAGACCAACATGCT-AAAAGCTGTC 2049  
Db 42040 CAGATCACTGGCTAGGACTCAAGACCAACCTGGCAACATGTAAGCTTC 42099

Qy 2050 TAGTAAATGCAAAATTCGTTGGCTGGGTGACTGTGTCCCAGTTACTTG 2109  
Db 42100 TACTAAAGTACAAAAAATTCGCTGGCTGTGTGGGTGCTGTAATCCCAGCTATICA 42159

Qy 2110 GGAGGCTGAGSTGGGAGGATCTTTAACCCCCAGGAGTTCAAGGCTCATGGCTGTGTGAT 2169

Search completed: April 12, 2003, 20:46:13  
Job time : 517.207 secs